



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153506756-5678-199370517911.BLASTQ4

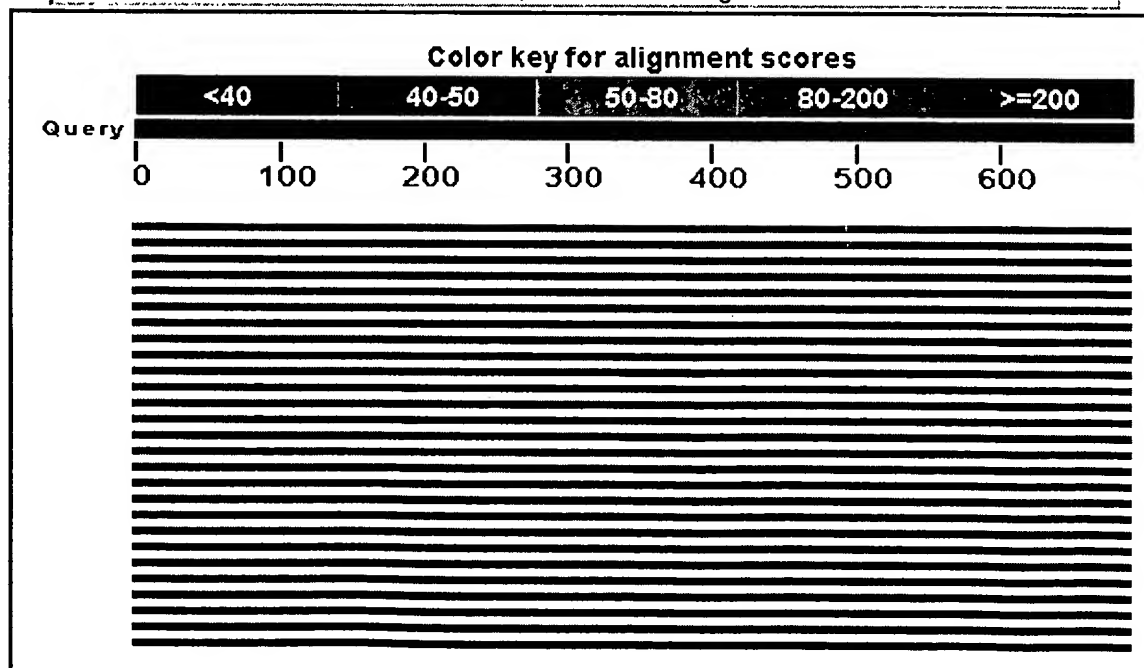
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
3,805,897 sequences; 1,312,134,661 total letters

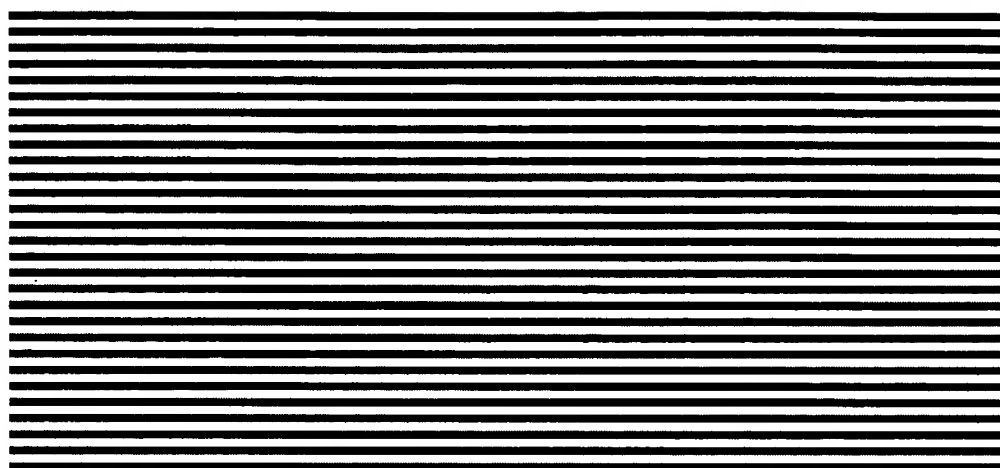
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=685

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments





[Distance tree of results](#) [Related Structures](#)

Sequences producing significant alignments:		Score (Bits)	E Value
gi 130455 sp P26664 POLG HCV1	Genome polyprotein [Contains: C...	1302	0.0
gi 14532249 gb AAK66556.1 	HCV type 1a/1b chimera polyprotein...	1302	0.0
gi 8926245 gb AAF81759.1 	polyprotein [Hepatitis C virus]	1301	0.0
gi 14532251 gb AAK66557.1 	HCV type 1a/1b chimera mutant polypro	1299	0.0
gi 329876 gb AAA45677.1 	polyprotein	1297	0.0
gi 63079188 gb AAV29640.1 	polyprotein [Hepatitis C virus]	1287	0.0
gi 55275808 gb AAV49742.1 	polyprotein [Hepatitis C virus]	1286	0.0
gi 48479030 gb AAT44836.1 	polyprotein [Hepatitis C virus]	1286	0.0
gi 22129793 ref NP_671491.1 	polyprotein [Hepatitis C virus] ...	1286	0.0
gi 6010588 gb AAF01182.1 	polyprotein [synthetic construct] >...	1285	0.0
gi 6010586 gb AAF01181.1 	polyprotein [synthetic construct] >...	1285	0.0
gi 9930557 gb AAG02099.1 	polyprotein [Hepatitis C virus]	1284	0.0
gi 2327071 gb AAB67036.1 	polyprotein [Hepatitis C virus strain	1283	0.0
gi 63079190 gb AAV29641.1 	polyprotein [Hepatitis C virus]	1283	0.0
gi 55275810 gb AAV49743.1 	polyprotein [Hepatitis C virus]	1282	0.0
gi 63079194 gb AAV29643.1 	polyprotein [Hepatitis C virus]	1281	0.0
gi 2327075 gb AAB67038.1 	polyprotein [Hepatitis C virus strain	1280	0.0
gi 9843677 emb CAC03609.1 	unnamed protein product [Hepatitis C	1278	0.0
gi 221587 dbj BAA01582.1 	polyprotein precursor [Hepatitis C vir	1278	0.0
gi 63079186 gb AAV29639.1 	polyprotein [Hepatitis C virus]	1278	0.0
gi 2327073 gb AAB67037.1 	polyprotein [Hepatitis C virus strain	1278	0.0
gi 63079196 gb AAV29644.1 	polyprotein [Hepatitis C virus]	1275	0.0
gi 130461 sp P27958 POLG HCVH	Genome polyprotein [Contains: C...	1268	0.0
gi 63079184 gb AAV29638.1 	polyprotein [Hepatitis C virus]	1263	0.0
gi 7650260 gb AAF65961.1 	polyprotein [Hepatitis C virus]	1234	0.0
gi 11559457 dbj BAB18808.1 	polyprotein [Hepatitis C virus]	1234	0.0
gi 7650232 gb AAF65947.1 	polyprotein [Hepatitis C virus]	1233	0.0
gi 5918947 gb AAD56189.1 	polyprotein [Hepatitis C virus]	1233	0.0
gi 5918965 gb AAD56198.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 130458 sp P26663 POLG HCVBK	Genome polyprotein [Contains: ...	1232	0.0
gi 12831193 gb AAK08509.1 	polyprotein [Hepatitis C virus type 1	1232	0.0
gi 7650246 gb AAF65954.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 5918945 gb AAD56188.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 7650244 gb AAF65953.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5918939 gb AAD56185.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5918937 gb AAD56184.1 	polyprotein [Hepatitis C virus]	1231	0.0

gi 46560636 gb AAT00644.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 23957857 gb AAD44718.2 	polyprotein [Hepatitis C virus]	1231	0.0
gi 7650266 gb AAF65964.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5821155 dbj BAA83719.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 87080431 emb CAH64686.1 	polyprotein [Hepatitis C virus]	1231	0.0
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gi 11559469 dbj BAB18814.1 	polyprotein [Hepatitis C virus]	1230	0.0
gi 48237634 gb AAT40682.1 	polyprotein [Hepatitis C virus]	1230	0.0
gi 1212742 dbj BAA08120.1 	HCV polyprotein [Hepatitis C virus]	1230	0.0
gi 7650248 gb AAF65955.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 7650236 gb AAF65949.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5918951 gb AAD56191.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 266820 sp Q00269 POLG HCVJT	Genome polyprotein [Contains: ...	1229	0.0
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gi 11559447 dbj BAB18803.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5918949 gb AAD56190.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5441839 emb CAB46915.1 	non-structural polyprotein [Hepati...	1229	0.0
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gi 7650256 gb AAF65959.1 	polyprotein [Hepatitis C virus]	1228	0.0
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gi 11559445 dbj BAB18802.1 	polyprotein [Hepatitis C virus]	1227	0.0
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gi 5918931 gb AAD56181.1 	polyprotein [Hepatitis C virus]	1226	0.0
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gi 5918963 gb AAD56197.1 	polyprotein [Hepatitis C virus]	1216	0.0
gi 5918961 gb AAD56196.1 	polyprotein [Hepatitis C virus]	1216	0.0
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gi 56342233 dbj BAD73994.1 	polyprotein [Hepatitis C virus type	1215	0.0
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gi 15529111 qb AAK97744.1	polyprotein [Hepatitis C virus]	1213	0.0
gi 3098644 qb AAC15727.1	polyprotein [Hepatitis C virus]	1213	0.0
gi 3098639 qb AAC15725.1	polyprotein [Hepatitis C virus]	1213	0.0
gi 1814090 dbj BAA09075.1	polyprotein [Hepatitis C virus]	1212	0.0
gi 56342207 dbj BAD73981.1	polyprotein [Hepatitis C virus type	1212	0.0
gi 3098646 qb AAC15728.1	polyprotein [Hepatitis C virus]	1212	0.0
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gi 3810874 dbj BAA20975.1	precursor polyprotein [Hepatitis C vi	1211	0.0
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gi 3098642 qb AAC15726.1	polyprotein [Hepatitis C virus]	1210	0.0
gi 3098655 qb AAC15732.1	polyprotein [Hepatitis C virus]	1210	0.0
gi 80322850 qb ABB52627.1	polyprotein [Hepatitis C virus]	1209	0.0
gi 2943784 dbj BAA25076.1	polyprotein [Hepatitis C virus]	1207	0.0
gi 81960062 sp Q913D4 POLG	HCVIN Genome polyprotein [Contains...	1207	0.0
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gi 306287 qb AAA45721.1	putative	1199	0.0
gi 50235322 qb AAT69968.1	polyprotein [Hepatitis C virus]	1199	0.0
gi 567060 qb AAA52748.1	polyprotein	1198	0.0
gi 5748511 emb CAB53095.1	polyprotein [Hepatitis C virus type 1	1197	0.0
gi 437108 qb AAA75355.1	polyprotein	1197	0.0
gi 7650258 qb AAF65960.1	polyprotein [Hepatitis C virus]	1195	0.0
gi 4753721 emb CAB41951.1	polyprotein [Hepatitis C virus]	1193	0.0
gi 7650262 qb AAF65962.1	polyprotein [Hepatitis C virus]	1193	0.0
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gi 67810846 qb AAY82011.1	polyprotein [Hepatitis C virus]	1174	0.0
gi 67810857 qb AAY82016.1	polyprotein [Hepatitis C virus]	1172	0.0
gi 67810849 qb AAY82012.1	polyprotein [Hepatitis C virus]	1172	0.0
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gi 67810842 qb AAY82009.1	polyprotein [Hepatitis C virus]	1170	0.0
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gi 67810855 qb AAY82015.1	polyprotein [Hepatitis C virus]	1169	0.0
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gi 67810868 qb AAY82021.1	polyprotein [Hepatitis C virus]	1168	0.0
gi 67810883 qb AAY82028.1	polyprotein [Hepatitis C virus]	1167	0.0
gi 28921568 ref NP_803144.1	NS3 protease/helicase' [Hepatitis C	1167	0.0
gi 67810881 qb AAY82027.1	polyprotein [Hepatitis C virus]	1167	0.0
gi 67810887 qb AAY82030.1	polyprotein [Hepatitis C virus]	1167	0.0
gi 67810844 qb AAY82010.1	polyprotein [Hepatitis C virus]	1166	0.0
gi 67810870 qb AAY82022.1	polyprotein [Hepatitis C virus]	1165	0.0
gi 67810851 qb AAY82013.1	polyprotein [Hepatitis C virus]	1165	0.0
gi 67810896 qb AAY82034.1	polyprotein [Hepatitis C virus]	1164	0.0
gi 67810861 qb AAY82018.1	polyprotein [Hepatitis C virus]	1163	0.0
gi 67810894 qb AAY82033.1	polyprotein [Hepatitis C virus]	1162	0.0
gi 67810864 qb AAY82019.1	polyprotein [Hepatitis C virus]	1162	0.0
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gi 68012706 qb AAY84749.1	nonstructural protein 3 [Hepatitis...	1160	0.0
gi 68012748 qb AAY84770.1	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012732 qb AAY84762.1	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012726 qb AAY84759.1	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012712 qb AAY84752.1	nonstructural protein 3 [Hepatitis C	1159	0.0
gi 68012752 qb AAY84772.1	nonstructural protein 3 [Hepatitis...	1159	0.0
gi 68012708 qb AAY84750.1	nonstructural protein 3 [Hepatitis C	1159	0.0
gi 68012698 qb AAY84745.1	nonstructural protein 3 [Hepatitis C	1159	0.0

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gi 68012714 qb AAY84753.1 	nonstructural protein 3 [Hepatitis C	1158	0.0
gi 68012746 qb AAY84769.1 	nonstructural protein 3 [Hepatitis C	1158	0.0
gi 68012744 qb AAY84768.1 	nonstructural protein 3 [Hepatitis C	1158	0.0
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gi 68012710 qb AAY84751.1 	nonstructural protein 3 [Hepatitis C	1157	0.0
gi 68012722 qb AAY84757.1 	nonstructural protein 3 [Hepatitis C	1156	0.0
gi 68012740 qb AAY84766.1 	nonstructural protein 3 [Hepatitis C	1155	0.0
gi 89519405 qb ABD75824.1 	polyprotein [Hepatitis C virus]	1155	0.0
gi 89519409 qb ABD75826.1 	polyprotein [Hepatitis C virus]	1154	0.0
gi 68012694 qb AAY84743.1 	nonstructural protein 3 [Hepatitis C	1153	0.0
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gi 89519413 qb ABD75828.1 	polyprotein [Hepatitis C virus]	1151	0.0
gi 89519407 qb ABD75825.1 	polyprotein [Hepatitis C virus]	1151	0.0
gi 89519415 qb ABD75829.1 	polyprotein [Hepatitis C virus]	1150	0.0
gi 89519411 qb ABD75827.1 	polyprotein [Hepatitis C virus]	1150	0.0
gi 81924266 sp O91936 POLG	HCVSA Genome polyprotein [Contains...	1150	0.0
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gi 93102504 qb ABE98154.1 	polyprotein [Hepatitis C virus subtyp	1144	0.0
gi 93102494 qb ABE98149.1 	polyprotein [Hepatitis C virus subtyp	1142	0.0
gi 81985682 sp Q5I2N3 POLG	HCV6A Genome polyprotein [Contains...	1142	0.0
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gi 93102502 qb ABE98153.1 	polyprotein [Hepatitis C virus subtyp	1140	0.0
gi 93102514 qb ABE98159.1 	polyprotein [Hepatitis C virus subtyp	1139	0.0
gi 93102496 qb ABE98150.1 	polyprotein [Hepatitis C virus subtyp	1139	0.0
gi 93102512 qb ABE98158.1 	polyprotein [Hepatitis C virus subtyp	1138	0.0
gi 93102508 qb ABE98156.1 	polyprotein [Hepatitis C virus subtyp	1138	0.0
gi 469213 dbj BAA05975.1 	fusion protein, composed of HCV p21...	1137	0.0
gi 93102516 qb ABE98160.1 	polyprotein [Hepatitis C virus subtyp	1134	0.0
gi 3550761 dbj BAA32665.1 	polyprotein [Hepatitis C virus (is...	1134	0.0
gi 93102506 qb ABE98155.1 	polyprotein [Hepatitis C virus subtyp	1133	0.0
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gi 62362180 qb AAX81527.1 	polyprotein [Hepatitis C virus]	1130	0.0
gi 82617874 qb ABB84854.1 	polyprotein precursor [Hepatitis C vi	1130	0.0
gi 82617878 qb ABB84856.1 	polyprotein precursor [Hepatitis C vi	1129	0.0
gi 82617876 qb ABB84855.1 	polyprotein precursor [Hepatitis C vi	1129	0.0
gi 81921385 sp O39928 POLG	HCVEV Genome polyprotein [Contains...	1127	0.0
gi 81921384 sp O39927 POLG	HCVEU Genome polyprotein [Contains...	1122	0.0
gi 3550765 dbj BAA32667.1 	polyprotein [Hepatitis C virus (is...	1121	0.0
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gi 67810998 qb AAY82049.1 	polyprotein [Hepatitis C virus]	1120	0.0
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gi 67810992 qb AAY82046.1 	polyprotein [Hepatitis C virus]	1119	0.0
gi 67810990 qb AAY82045.1 	polyprotein [Hepatitis C virus]	1119	0.0
gi 67810986 qb AAY82043.1 	polyprotein [Hepatitis C virus]	1119	0.0
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gi 67811008 qb AAY82054.1 	polyprotein [Hepatitis C virus]	1118	0.0
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gi 67811012 qb AAY82056.1 	polyprotein [Hepatitis C virus]	1117	0.0

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gi 67811004 gb AAAY82052.1 	polyprotein [Hepatitis C virus]	1116	0.0
gi 89113921 gb AAV75597.2 	polyprotein precursor [Hepatitis C vi	1116	0.0
gi 67811030 gb AAAY82065.1 	polyprotein [Hepatitis C virus]	1115	0.0
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gi 67811065 gb AAAY82082.1 	polyprotein [Hepatitis C virus]	1109	0.0
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gi 33413949 gb AAP55700.1 	polyprotein [Hepatitis C virus]	1069	0.0
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gi 5616215 gb AAD45674.1	NS3 helicase [Hepatitis C virus]	814	0.0	
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gi 5031420 gb AAD38162.1	polyprotein [Hepatitis C virus]	811	0.0	
gi 5616212 gb AAD45673.1	NS3 helicase [Hepatitis C virus]	808	0.0	
gi 1372955 gb AAB02124.1	NS3 gene product	808	0.0	
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gi 83755049 pdb 2F55 C	Chain C, Two Hepatitis C Virus Ns3 Hel...	794	0.0	S
gi 4930270 pdb 8OHM	Crystal Structure Of Rna Helicase From ...	787	0.0	S
gi 793912 gb AAA65789.1	precursor protein	708	0.0	
gi 221620 dbj BAA03177.1	NS3-4 protein [Hepatitis C virus]	699	0.0	
gi 5353561 gb AAD42179.1	superoxide dismutase/HCV major epit...	535	2e-150	
gi 2731650 gb AAB93501.1	polyprotein [Hepatitis C virus]	519	2e-145	
gi 2731652 gb AAB93502.1	polyprotein [Hepatitis C virus]	502	2e-140	
gi 765334 gb AAB31751.1	c33-c antigen [Hepatitis C virus]	496	1e-138	
gi 221622 dbj BAA03178.1	NS3 protein [Hepatitis C virus]	488	5e-136	
gi 2160336 dbj BAA01515.1	ORF 1 [Hepatitis C virus]	484	7e-135	
gi 4433101 dbj BAA20994.1	NS3 protein [Hepatitis C virus]	472	2e-131	
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gi 2660983 gb AAB88168.1	polyprotein [Hepatitis C virus]	459	2e-127	

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gi 2660935 gb AAB88144.1 	polyprotein [Hepatitis C virus]	456	2e-126
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gi 2660975 gb AAB88164.1 	polyprotein [Hepatitis C virus]	444	7e-123
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gi 3157746 dbj BAA28501.1 	polyprotein [Hepatitis C virus]	407	1e-111
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gi 3157754 dbj BAA28505.1 	polyprotein [Hepatitis C virus]	403	2e-110
gi 3157740 dbj BAA28498.1 	polyprotein [Hepatitis C virus]	402	4e-110
gi 3157742 dbj BAA28499.1 	polyprotein [Hepatitis C virus]	401	5e-110
gi 3157748 dbj BAA28502.1 	polyprotein [Hepatitis C virus]	400	1e-109
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gi 33090378 gb AAP57528.1 	polyprotein [synthetic construct]	400	1e-109
gi 13162188 emb CAC33083.1 	polyprotein [Hepatitis GB virus B]	400	2e-109
gi 9628102 ref NP_056931.1 	polyprotein [Hepatitis GB virus B...	400	2e-109
gi 21727887 emb CAD21957.1 	non-structural polyprotein [Hepatiti	397	8e-109
gi 3157802 dbj BAA28529.1 	polyprotein [Hepatitis C virus] >g...	396	2e-108

Alignments

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Deselect all

Distance tree of results

> [gi|130455|sp|P26664|POLG](#) HCV1 Genome polyprotein [Contains: Core protein p21 (Caps: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|329874|gb|AAA45676.1|](#) HCV-1
Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTITITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTITITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]
gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
 Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.
 Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|8926245|gb|AAF81759.1| polyprotein [Hepatitis C virus]
 Length=3011

Score = 1301 bits (3366), Expect = 0.0, Method: Composition-based stats.
 Identities = 682/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240

Sbjct	1207	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|14532251|gb|AAK66557.1| HCV type 1a/1b chimera mutant polyprotein [synthetic cor
Length=3011

Score = 1299 bits (3362), Expect = 0.0, Method: Composition-based stats.
Identities = 681/685 (99%), Positives = 682/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPPVVPQSFQVAHLHAPTGS +TKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPPVVPQSFQVAHLHAPTGSAAATKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVSTWVlvvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHPVTKYIMTMSADLEVVSTWVVLVGGVLAALAAAYCLSTGCVVIVGRV	
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTMSADLEVVSTWVVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|329876|gb|AAA45677.1| polyprotein
Length=2436

Score = 1297 bits (3357), Expect = 0.0, Method: Composition-based stats.
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	577	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	636
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	637	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	696
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	697	DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	756
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF TDNSSPPVVPQSFQVAHLHAPTGS GSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	757	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	816
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	817	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	876
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	877	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	936
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP PIGDVVVVATDALMTGYTG	420

Sbjct	937	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	996
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	997	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1056
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1057	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1116
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1117	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1176
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1177	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	1236
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 VLSGKPAIIPDREVL YREFDEMEEC	
Sbjct	1237	VLSGKPAIIPDREVL YREFDEMEEC 1261	

> gi|63079188|gb|AA29640.1| polyprotein [Hepatitis C virus]
Length=2889

Score = 1287 bits (3331), Expect = 0.0, Method: Composition-based stats.
Identities = 672/685 (98%), Positives = 681/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQ+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGsllsprPISYLGSSGGPLLCPAGHAVG+FAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGsllsprPISYLGSSGGPLLCPAGHAVGVFAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP PPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVA+G+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVAMGVNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		VLSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC	1711

>gi|55275808|gb|AAV49742.1| polyprotein [Hepatitis C virus]
Length=2742

Score = 1286 bits (3329), Expect = 0.0, Method: Composition-based stats.
Identities = 673/685 (98%), Positives = 679/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTI+T TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIDTSTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600




		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC	685
		VLSGKPAIIPDREVL YREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVL YREFDEMEEC	1711

> [gi|48479030|gb|AAT44836.1|](#) polyprotein [Hepatitis C virus]
Length=2908

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
Identities = 670/685 (97%), Positives = 680/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrg	120
		TRTIASPKGPVIQMYTN+DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNIDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVI+GR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIIGRI	1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 VLSGKPA+IPDREVLRYREFDEMEEC
 Sbjct 1687 VLSGKPAVIPDREVLRYREFDEMEEC 1711

>  gi|22129793|ref|NP_671491.1|  polyprotein [Hepatitis C virus]
 gi|2316098|gb|AAB66324.1|  polyprotein [Hepatitis C virus]
 Length=3011

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
 Identities = 670/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		VLSGKPAIIPDREVLRY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYQEFDEMEEC 1711	

> gi|6010588|gb|AAF01182.1| polyprotein [synthetic construct]
gi|6010584|gb|AAF01180.1| polyprotein [synthetic construct]
 Length=3015

Score = 1285 bits (3324), Expect = 0.0, Method: Composition-based stats.
 Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1031	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1090
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1091	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1151	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTTMR	1210
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1211	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1271	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1391	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1451	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1631	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1690
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1691	VLSGKPAIIPDREVLYQEFDEMEEC	1715

> gi|6010586|gb|AAF01181.1| polyprotein [synthetic construct]
gi|6010582|gb|AAF01179.1| polyprotein [synthetic construct]
 Length=3015

Score = 1285 bits (3324), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS	SLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1031	APITAYAQQTRGLLGCIITS	SLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	1090
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS	LTPTCTGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1091	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS	LTPTCTGSSDLYLVTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGP	LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1151	DSRGSLLSPRPISYLGSSGGP	LLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTTMR	1210
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPT	TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1211	SPVFETDNSSPPVPQSFQVAHLHAPT	TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTIT	TGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1271	YMSKAHGIDPNIRTGVRTIT	TGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1330
Query	301	LGIGTVLDQAETAGARLV	LATATPPGSVTVHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1331	LGIGTVLDQAETAGARLV	LATATPPGSVTVHPNIEEVALSTTGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKKDELA	AKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	420
Sbjct	1391	GGRHLIFCHSKKKKDELA	AKLVALGINAVAYYRGLDVSVIP TSGDVVVVSTDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVD	FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1451	DFDSVIDCNTCVTQTVD	FSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1510
Query	481	RPSGMFDSSVLCECYDAG	CAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEDEVFTGLT	540
Sbjct	1511	RPSGMFDSSVLCECYDAG	CAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEDEVFTGLT	1570
Query	541	HIDAHFLSQTKQSGEN	PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP	600
Sbjct	1571	HIDAHFLSQTKQSGEN	PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP	1630
Query	601	RLGAVQNEITLTHPV	TKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
Sbjct	1631	RLGAVQNEITLTHPV	TKYIMTCMSADLEVVTSTWVLVGGVLAALAAYCLSTGCVVIVGR+	1690
Query	661	VLSGKPAIIPDREVL	YREFDEMEEC 685	
Sbjct	1691	VLSGKPAIIPDREVL	YQEFDEMEEC 1715	

>gi|9930557|gb|AAG02099.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1284 bits (3322), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS	SLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITS	SLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVRR+G	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVG+FRFAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFD VIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCMSA+ EVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLY+EFDEMEEC	1711

> gi|2327071|gb|AAB67036.1| polyprotein [Hepatitis C virus strain H77]
Length=3011

Score = 1283 bits (3321), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGT TMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDVVW+TDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTT IETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTT IET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTT IETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGEN PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

>gi|63079190|gb|AA29641.1| polyprotein [Hepatitis C virus]

Length=2885

Score = 1283 bits (3321), Expect = 0.0, Method: Composition-based stats.
Identities = 673/685 (98%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMS+AHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAIQATVCARAQAPPPSWDQMWKCLRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC	1711

>gi|55275810|gb|AAV49743.1| polyprotein [Hepatitis C virus]
Length=2742

Score = 1282 bits (3318), Expect = 0.0, Method: Composition-based stats.
Identities = 670/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLE IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLV LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVVLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTI+ TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIDISTLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 VLSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC 1711	

> [gi|63079194|gb|AA29643.1|](#) polyprotein [Hepatitis C virus]

Length=2883

Score = 1281 bits (3315), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTDATS+	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446

Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQ E+TLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQTEVTLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYREFDEMEEC	1711

> [gi|2327075|gb|AAB67038.1|](#) polyprotein [Hepatitis C virus strain H77]
Length=3011

Score = 1280 bits (3312), Expect = 0.0, Method: Composition-based stats.
Identities = 667/685 (97%), Positives = 675/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY QQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYTQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLLPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLL PCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLLAPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQSGEN PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQSGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|9843677|emb|CAC03609.1| unnamed protein product [Hepatitis C virus]
Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
Identities = 666/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAV+F+PVENLETTMR	180
Sbjct	1147	DGRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVEFVPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNS+PP VPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSAPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCD+LAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDDLAAKLVALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDS+VLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSAVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHG TPLLY	600
Sbjct	1567	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGSTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIMTCMSADLE+VTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKP IIPD+EVLYREFDEMEEC	1711

> gi|221587|dbj|BAA01582.1| polyprotein precursor [Hepatitis C virus]
Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
Identities = 665/685 (97%), Positives = 674/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPAGH VGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATS+	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPH NIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDfSLDPTFTTITETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDfSLDPTFTTITET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSS+LCECYD GCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ GEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQ E+TLTHPVTKYIMTCMSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685

VLSG+PAIIPDREVLRYREFDEMEEC
 Sbjct 1687 VLSGRPAIIPDREVLRYREFDEMEEC 1711

> gi|63079186|gb|AA29639.1| polyprotein [Hepatitis C virus]
 Length=2889

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
 Identities = 669/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQ ETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQXETAGARLVVLATATPPGSVTVPHXNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKLV LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKVTLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCN CVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNICVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLRYREFDEMEEC 1711	

> gi|2327073|gb|AAB67037.1| polyprotein [Hepatitis C virus strain H77]
 Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
Identities = 667/685 (97%), Positives = 675/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLT RDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLT SRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGT TMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDN SPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNPSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> [gi|63079196|gb|AAI29644.1|](#) polyprotein [Hepatitis C virus]
Length=2889

Score = 1275 bits (3300), Expect = 0.0, Method: Composition-based stats.
Identities = 668/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIV TAAQTFLATCINGVCWTVYHGAG	

Sbjct	1027	APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVXTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQM TNV+QDL+GWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS TVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIMTCSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	LSGKPAIIPDREVLYREFDEMEEC	1711

> [gi|130461|sp|P27958|POLG_HCVH](#) Genome polyprotein [Contains: Core protein p21 (Capsid) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|329738|gb|AAA45534.1|](#) polyprotein
 Length=3011

Score = 1268 bits (3281), Expect = 0.0, Method: Composition-based stats.
 Identities = 663/685 (96%), Positives = 672/685 (98%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

Sbjct	1027	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQ YTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQTYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCP GHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAA+GYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAKGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTGSPITYSTY GKFLAD GCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTY GKFLADAGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK GIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	SGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLFEWGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHL FEWGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLGFEWGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQM KCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMRKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|63079184|gb|AA29638.1| polyprotein [Hepatitis C virus]
Length=2882

Score = 1263 bits (3268), Expect = 0.0, Method: Composition-based stats.
Identities = 661/685 (96%), Positives = 674/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIA+PKGPVIQMYTNVDQDLVGWPAPQG+RSLTPC CGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIATPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCACGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKCHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPLELIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSK+KC++LAALKLVA G+NAVAYYRGLDVSVIP G+VVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	+FDSVIDCNTCVTQTVDFSLDPTF IET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIMTCSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|7650260|gb|AAE65961.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1234 bits (3193), Expect = 0.0, Method: Composition-based stats.
Identities = 636/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTYVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|11559457|dbj|BAB18808.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1234 bits (3193), Expect = 0.0, Method: Composition-based stats.
Identities = 635/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA KLVALG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELATKLVALGVNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNDVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|7650232|gb|AAF65947.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1233 bits (3190), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSF LATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGP LCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGP LCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVPQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPT GSGKST+VPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPT GSGKSTRVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTG+RTIT TGG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGIRTIT TGGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAACL ALGINAV+YYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAACL SALGINAVSYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTQKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVT KYIMTCMSADLEVVTSTWvlvggvlaalaa YCLSTGCVVIVGRV RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITK FIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 +LSG+PAIIPDRE LY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREALYQEFDEMEEC 1711	

> [gi|5918947|gb|AAD56189.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1233 bits (3189), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGILLSPRP+SYLGSSGGP LCP GH VG+FAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGILLSPRPVSYLGSSGGP LCP LGHVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTIT TGG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTIT TGGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE+IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEIIK	1386
Query	361	GGRHLIFCHSKKKKCELAACL VALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAACL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAACL SALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	TLSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|5918965|gb|AAD56198.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1232 bits (3188), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDFIPVE++ET+MR	
Sbjct	1147	DSRGSLLSPRPISYLKGSSGGPLLCPGLGHVVGIFRAAVCTRGVAKAVDFIPVESMETSMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEAALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA+KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAASKLSALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct	1567	HIDAHFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP LHGPTPLLY HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TK+IMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKFIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLRYREFDEMEEC 1711	

> gi|130458|sp|P26663|POLG_HCVBK Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
gi|329771|gb|AAA72945.1| [Hepatitis C virus core, matrix, envelope and non-structural protein RNA.], gene product
 Length=3010

Score = 1232 bits (3188), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A+PKGP+ QMYTNVDQDLVGWP P G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAAPKGPITQMYTNVDQDLVGWPKPPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLGSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPFGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG+P+TYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGAPVITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALK LGINAVAYYRGLDVSVIP IGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtgrgrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PAI+PDRE+LY+EFDEMEEC	
Sbjct	1687	ILSGRPAIVPDRELLYQEFDEMEEC	1711

>gi|12831193|gb|AAK08509.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVFTDNSSPP VPPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+P+TYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPVTYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LGINAVAYYRGLDVSVIP IGDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGINAVAYYRGLDVSVIPITIGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTT IETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTT IET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTT IETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660

Sbjct 1627 RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSG+PAI+PDRE+LY+EFDEMEEC
 Sbjct 1687 ILSGRPAIVPDRELLYQEFDEMEEC 1711

> [gi|7650246|gb|AAF65954.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
 Identities = 635/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG
 Sbjct 1027 APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg 120
 ++T+A PKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPVIQMYTNVDQDLVGWPAPPGARSRLTPCTCGSSDLYLVRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR
 Sbjct 1147 DSRGSLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G+DPNIRTGVRTITTTG+ ITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI
 Sbjct 1267 YMSKAYGVDPNIRTGVRTITTTGASITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLETIK 1386

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG
 Sbjct 1387 GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG 1446

Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLPODAVSrtqrrgrtgryKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWD MWKCL RLKPTLHGPTPLLY
 Sbjct 1567 HIDAFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDLMWKCLTRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPAIIPDREVLYREFDEMEEC
 Sbjct 1687 ILSGKPAIIPDREVLYREFDEMEEC 1711

> gi|5918945|gb|AAD56188.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP GHAVG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPLGHAVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE+IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEIIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	TLSGRPAIIPDREVLYQEFDEMEEC 1711	

> gi|7650244|gb|AAF65953.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.

Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCP LGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSALGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		+FDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	NFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPA+IPDREVL YREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVL YREFDEMEEC 1711	

> [gi|5918939|gb|AAD56185.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.
 Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWQAPPGSRSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+ VIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIGVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA+IPDRE+LYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREILYREFDEMEEC	1711

> gi|5918937|gb|AAD56184.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWQAPPGSRSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	

Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP V PQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDII+CDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIGVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIP GDV VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSALGLNAVAYYRGLDVSVIPTSGDV VVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTT IETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTT IET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSG+PA+IPDRE+LYREFDEMEEC 1711	

>gi|46560636|gb|AAT00644.1| polyprotein [Hepatitis C virus]
Length=3014

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1031	APITAY+QQTRGLLGCI+TSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1090
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYL VTRHADVIPVrrrg	120
Sbjct	1091	++T+A PKGP+IQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYL VTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1151	DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1210
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1211	SPVFTDNSSPP V PQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1270

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1271	YMSKAYGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIMCDECHSTDSTSI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHP+IEEVALS GEIPFYGKAIP+EVIK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNIGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1391	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1450
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1451	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTMPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQAGENFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1631	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1690
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		VLSGKPAIIPDRE LY+EFDEMEEC	
Sbjct	1691	VLSGKPAIIPDREALYQEFDEMEEC 1715	

> [gi|23957857|gb|AAD44718.2|](#) polyprotein [Hepatitis C virus]
 Length=3015

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPVIAQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKGS SGGPLLCP+GHAVG+FRFAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1148	DNRGSLLSPRPVSYLKGS SGGPLLCPSGHAVGVFRFAAVCTRGVAKAVDFVPVESMETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKST+VPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTRVPAAYAAQGYKVLVNLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1268	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIMCDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	

Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1387
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1388	GGRHLIFCHSKKKKCELAALKSLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1447
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTGTGSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1688	ILSGRPAVVPDREVLRYREFDEMEEC 1712	

> [gi|7650266|gb|AAF65964.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTNRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTNRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTNRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSCGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTYKFLADGGCSCGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSCGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLN LGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

>gi|5821155|dbj|BAA83719.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 635/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLG IITSLTGRDKN+VEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGSIITSLTGRDKNRVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLT CTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTSCCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1148	DSRGSLLSPRPVSYLKSSGGPLLCPSGHTVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1207
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1208	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1268	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1387
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA AKL ALGINAVAYYRGLDVSVIP GD VVVATDALMTGYTG	
Sbjct	1388	GGRHLIFCHSKKKKDELA AKLSALGINAVAYYRGLDVSVIPTSGDAVVVVATDALMTGYTG	1447
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSV DCNTCVTQTVDFSLDPTFTTET T+PQD+VSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVTD CNTCVTQTVDFSLDPTFTTETTTVPQDSVSRSQRRGRTGRGRGGIYRFVIPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	

Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSG+PAIIPDREVLVREFDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVLVREFDEMEEC 1712	

> gi|87080431|emb|CAH64686.1| polyprotein [Hepatitis C virus]
 Length=3011

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVST +QTFLATC+NGVCWTVYHGAG	
Sbjct	1028	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTTSQTFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+++A PKGP++QMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	AKSLAGPKGPILQMYTNVDQDLVGWPAPQGTSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ET MR	
Sbjct	1148	DTRGSLLSPRPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETVMR	1207
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP FTDNS+PP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1208	SPTFTDNSTPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1268	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAET GAR+VVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIPLEVIK	
Sbjct	1328	LGIGTVLDQAETCGARMVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPLEVIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL +LG+NAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKCDELA AKLTSGLNAVAYYRGLDVSVIPLSGDVVVVSTDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTITETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCN CVTQTVD FSLDPTFTTITET TLPQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNVCVTQTVD FSLDPTFTTITETTTLPQDAVSRSQRRGRTGRGRLGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAYMNTPLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYMNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA APPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARASAPPPSWDQMWKCLIRLKPTLRGPTPLLY	1627

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGG+LAALAAAYCLSTG VVIVGR+	
Sbjct	1628	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGILAAALAAAYCLSTGSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1688	VLSGKPAIIPDREVLYKEFDEMEEC	1712

> [gi|5918967|gb|AAD56199.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1230 bits (3183), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPTCTGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP GH VGIFRAAVCTRGVAKAVDFIPVE++ET+MR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCP LGHVVGIFRAAVCTRGVAKAVDFIPVESMETSMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA+KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAASKLSALGVNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQ KQ+G+N PYLVAIYQATVCARAQAPPPSWDMWKCLIRLKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQNKQAGDNFPYLVAIYQATVCARAQAPPPSWDMWKCLIRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITK FIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PAIIPDREVLYREFDEMEEC	

Sbjct 1687 ILSGRPAPIPDREVLRYREFDEMEEC 1711

> gi|11559469|dbj|BAB18814.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1230 bits (3183), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIIVTSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLSLPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLGSSGGPLLCPSGHIVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+ IITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGASITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LGINAVAYYRGLDVSVIP G+VVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSLGINAVAYYRGLDVSVIPASGNVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPA+IPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLRYREFDEMEEC 1711	

> gi|48237634|gb|AAT40682.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1230 bits (3182), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVS+IP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA+APPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAKAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> [gi|1212742|dbj|BAA08120.1|](#) HCV polyprotein [Hepatitis C virus]
Length=3010

Score = 1230 bits (3182), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP+GH VGI FRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVS+IP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARA+APPPSWDQMWKCLIRLKPRTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAKAPPPSWDQMWKCLIRLKPRTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> [gi|7650248|gb|AAF65955.1|](#) polyprotein [Hepatitis C virus]

Length=3010

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+IQMYTNVD DLVGW P G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPPIQMYTNVDLDLVGWQVPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR DSRGSLLSPRPVSYLKSSGGPLLCP LGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPV+TDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVYTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVR ITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCAR+QAPPPSWDQMWKCL+RL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARSQAPPPSWDQMWKCLLRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|7650236|gb|AAF65949.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPV RRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVHRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T++	
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLC+CYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCDCYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> [gi|5918951|gb|AAD56191.1](#) polyprotein [Hepatitis C virus]
 Length=3013

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
 Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1030	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1089
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADV+PVRRRG	
Sbjct	1090	AKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVVPVRRRG	1149
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKGS SGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1150	DSRGSLLSPRPVSYLKGS SGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1209
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1210	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1269
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1270	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1329
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1330	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVI+ LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP+EVIR	1389
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1390	GGRHLIFCHSKKKKCELATKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1449
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1450	DFDSVIDCNCVTQTQTVDFSLDPTFTTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1509
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1510	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1569
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1570	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1629
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1630	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1689
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1690	ILSGRPAVIPDREVLYQEFDEMEEC 1714	

> [gi|266820|sp|Q00269|POLG_HCVJT](#) Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|221613|dbj|BAA01943.1|](#) polyprotein [Hepatitis C virus]
[gi|384057|prf|1904413A](#) polyprotein
 Length=3010

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWHAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVV+VATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSGLGINAVAYYRGLDVSVIPTSGDVVIVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvjgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC	685
		+LSG+PA++PDREVLVREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLVREFDEMEEC	1711

> [gi|464178|dbj|BAA03581.1|](#) polyprotein [Hepatitis C virus (isolate HC-G9)]
[gi|81992806|sp|Q81754|POLG_HCVH9](#) Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3011

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
 Identities = 635/685 (92%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+RTIAS GPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCG+SDLYLVTRHADVIPVRRRG	
Sbjct	1087	SRTIASASGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGASDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLC PAGHVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLC PHAVGIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLC PMGHAVGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPTVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTGSPIT+STYGKFLADGGCSGGAYDIIICDECHS DATSI	

Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGSPITHSTYKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL +LATATPPGSVTVPH NIEEVALST GEIPFYGKAIPL IK	
Sbjct	1327	LGIGTVLDQAETAGVRLTILATATPPGSVTVPHSNIEEVALSTEGEIPFYGKAIPLNYIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKV LG+NAVA+YRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVGLGVNAVAFYRGLDVSVIPPTGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVSLDPTFTIETITLPODAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	
Sbjct	1447	DFDSVIDCNTCVVQTVDFSLDPTFSIETSTVPQDAVSRQRRGRTGRGKHGIYRYVSPGE	1506
Query	481	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARA+APPPSWDQMWKCLIRLKPTL G TPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAQATVCARAKAPPPSWDQMWKCLIRLKPTLTGATPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV	660
		RLG VQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	
Sbjct	1627	RLGGVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSGKPA+IPDREVLVREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLVREFDEMEEC 1711	

> gi|11559447|dbj|BAB18803.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1229 bits (3180), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAH+HAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHIHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSNTGEIPFYGKAIPLEAIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGM DSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMLDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|5918949|gb|AAD56190.1| polyprotein [Hepatitis C virus]

Length=3013

Score = 1229 bits (3179), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1030	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1089
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADV+PVRRRG	
Sbjct	1090	AKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVVPVRRRG	1149
Query	121	dsrgsllsprPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGP L LCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1150	DSRGSLSPRPVS YLGSSGGP L LCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1209
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPT GSGKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1210	SPVF TDNSSPPAVPQTFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	1269
Query	241	YMSKAHGIDPNIRTGVRTIT T GSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTIT T G+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1270	YMSKAHGVDPNIRTGVRTIT T GAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTSI	1329
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVI+	
Sbjct	1330	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIR	1389
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1390	GGRHLIFCHSKKKKCELATKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1449
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1450	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGGIYRFVTPGE	1509
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1510	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1569
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1570	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1629
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1630	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1689
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1690	ILSGRPAIIPDREVLYQEFDEMEEC 1714	

> gi|5441839|emb|CAB46915.1| non-structural polyprotein [Hepatitis C virus]
gi|5441833|emb|CAB46911.1| non-structural polyprotein [Hepatitis C virus]
Length=2201

Score = 1229 bits (3179), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	218	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	277
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	278	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG	337
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	338	DSRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	397
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	398	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	457
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	458	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	517
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	
Sbjct	518	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTTGEIPFYGKAIPETIK	577
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	578	GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	637
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	638	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	697
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	698	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	757

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Query   541  HIDAHFSLQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAHFSLQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   758  HIDAHFSLQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  817

Query   601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV  660
          RLGAVQNE+T THP+TKYIM CMSADLEVVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   818  RLGAVQNEVTTHPITKYIMACMSADLEVVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI  877

Query   661  VLSGKPAIIPDREVLVREFDEMEEC  685
          +LSGKPAIIPDREVLVREFDEMEEC
Sbjct   878  ILSGKPAIIPDREVLVREFDEMEEC  902

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> [gi|5420377|emb|CAB46677.1|](#) polyprotein [Hepatitis C virus type 1b]
[gi|68565847|sp|Q9WMX2|POLG](#) HCVCO Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
Length=3010

Score = 1228 bits (3178), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

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Query    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG  60
          APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
Sbjct   1027 APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG  1086

Query    61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg  120
          ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   1087 SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG  1146

Query   121  dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR  180
          DSRGSLLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
Sbjct   1147 DSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR  1206

Query   181  SPVFETDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240
          SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   1207 SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  1266

Query   241  YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI  300
          YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I
Sbjct   1267 YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI  1326

Query   301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK
Sbjct   1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEIPFYGKAIPETIK  1386

Query   361  GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG
Sbjct   1387 GGRHLIFCHSKKKKCELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG  1446

Query   421  DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE  480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
Sbjct   1447 DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE  1506

Query   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT  540
          RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT

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Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLRYREFDEMEEC 1711	

> gi|62006147|dbj|BAD91386.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGFVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTQFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKA P+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAFFIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELATKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQEFDEMEEC	1711

> gi|5738247|gb|AAD50312.1| polyprotein precursor [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSALTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSALTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSALTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPN+RTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNLRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E+IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPIEIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIP G+VVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKSLGLLNAVAYYRGLDVSVIPTSGNVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPODAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNETTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	

Sbjct 1687 VLSGKPAIIPDREVLVYQEFDEMEEC 1711

> gi|7650228|gb|AAF65945.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPVIAQMYTNVDQDLVGWAAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPATIK	1386
Query	361	GGRHLIFCHSKKKKDELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAACL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAACLALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+URLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVURLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVYREFDEMEEC 685	
		+LSG+PA+IPDREVLVY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLVYQEFDEMEEC 1711	

> gi|5918957|gb|AAD56194.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

>gi|5918929|gb|AAD56180.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPPIAQMNTNVDQDLVGWAAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIP IATIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAACKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAACKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSG+PA+IPDREVLY+EFDEMEEC ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3176), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYAQQTRGLFGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRR SKTLAGPKGPITQMYTNVDQDLVGWQAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRRS	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	D RGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR DGRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPV+TDNSSPP VPQS FQVAHLHAPTGS GKST+VPAAYAAQGYKVLVLNPSVAATLGFG	240
Sbjct	1207	SPVYTDNSSPPAVPQS FQVAHLHAPTGS GKSTRVPAAYAAQGYKVLVLNPSVAATLGFGT	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVVATDALMTGYTG GGRHLIFCHSKKKKCELAAL+L ALGINAVAYYRGLDVS+IP GDV VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALQTALGINAVAYYRGLDVSIIPTSGDV VVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTTET T+PQD+VSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTVPQDSVSRSQRRGRTGRGRGGIYRYVIPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgg vlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TKYIM CMSADLE+VTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKYIMACMSADLEIVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYREFDEMEEC 1711	

> gi|7650222|gb|AAF65942.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3176), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPP GARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DTRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+++IK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKDELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
Sbjct	1687	+LSG+PA++PDREVLRY+FDEMEEC	1711

> gi|46560634|gb|AAT00643.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1227 bits (3175), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEI FYGKAIP+EVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEISFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITLPODAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHPVTKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSGKPA+IPDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLRYQEFDEMEEC 1711	

> gi|11559455|dbj|BAB18807.1 polyprotein [Hepatitis C virus]
Length=3011

Score = 1227 bits (3175), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1028	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1088	SKTLAGPKGPVTQMYTNVDQDLVGWQAPPGARSRLTPCTCGSSDLYLVRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPPLCP GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1148	DSRGSLLSPRPVSYLKSSGGPPLCPLGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTVGRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPN+RTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1268	YMSKAYGIDPNVRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	360
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1387
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA KL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1388	GGRHLIFCHSKKKKCELATKLSGLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1447

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVLYQEFDEMEEC 1712	

> [gi|7650240|gb|AAF65951.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIA SPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++ +A KGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKALAGQKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQS FQVAHLHAPT GSGKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPT GSGKSTKVPAAYA+QGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPT GSGKSTKVPAAYASQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYL AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLTAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA+IPDR+VLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDRDVLYQEFDEMEEC 1711	

> gi|11559451|dbj|BAB18805.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLKGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKGSSGGPLLCPLGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELATKLSALGINAVAYYRGLDVSVIP TSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTMPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+GENLPYLVAYQATVCARAQAPPPSWDQMWKCL+RLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGENLPYLVAYQATVCARAQAPPPSWDQMWKCLVRLKPTLQGPTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSG+PA++PDREVLY+EFDEMEEC	
Sbjct	1687	VLSGRPAVVPDREVLYQEFDEMEEC	1711

> gi|11559445|dbj|BAB18802.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAV+FIPVE++ETMR	
Sbjct	1147	DNRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVEFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKL+ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLLALGVNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G++ PYLVAQATVCARAQAPPPSWDMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDHFYPYLVAQATVCARAQAPPPSWDMWKCLRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCM+ADLE+ TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIIMTCMAADLEIATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685

+LSG+PA++PDREVLY+EFDEMEEC
 Sbjct 1687 ILSGRPAVVPDREVLYQEFDEMEEC 1711

> gi|471117|dbj|BAA01728.1| polyprotein precursor [Hepatitis C virus]
 Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVR+ADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSRLTPCTCGSSDLYLVRTRYADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKGSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPGSHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITITGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN RTGVRTITITG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNTRTGVRTITITGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|5918953|gb|AAD56192.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1226 bits (3173), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		Y+SKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YVSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAGKLSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET+T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETMTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlggvl aalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKLIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPVAVVPDREVLYREFDEMEEC 1711	

>gi|11559449|dbj|BAB18804.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3173), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGS SGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE +ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGS SGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG DPNIRTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKL +LGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSSLGINAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> [gi|2764398|emb|CAA03854.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VP++FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPETFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL LG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKSLGLLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYL AYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLTAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVVLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

> gi|56342187|dbj|BAD73971.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNVGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDREVLY++FDEMEEC 1711	

>gi|7341103|gb|AAF61205.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1025	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	1084
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1085	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1144
Query	121	dsrgsllsprPISYLKGSSGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1145	DSRGSLLSPRP+SYLKGSSGGPLLC P+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1204
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1205	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1264
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1265	YMSKAHG+DPNIRTG RT+TTG+PITYSTY GKFLADGGCSGGAYDII+CDECHSTD+TSI	1324

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1325	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1384
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1385	GGRHLIFCHSKKKCDELA TKLSGLGINAVAYYRGLDVSVIPASGNVVVVATDALMTGYTG	1444
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1445	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1504
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1505	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1564
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1565	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1624
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1625	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1684
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1685	ILSGKPAVIPDREVLYREFDEMEEC 1709	

> gi|7650234|gb|AAF65948.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVG+FAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGLFAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	

Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTI+T T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIDTTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQEFDEMEEC 1711	

> gi|5918955|gb|AAD56193.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		Y+SKAHGIDPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YVSKAHGIDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAGKLSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET+T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETMTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKLIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTGSVIVIGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLYREFDEMEEC 1711	

> gi|5918931|gb|AAD56181.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPPIAQMYTNVDQDLVGWAAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPATIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	

Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC	1711

> gi|266821|sp|P29846|POLG_HCVTW Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLFGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW APQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWHAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFDTNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFDTNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFDTNSSPPAVPQAFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALGI+AVAYYRGLDVSVIP G+VVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGIHAVAYYRGLDVSVIPASGNVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRT RG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTMPQDAVSRSQRRGRTSRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	

Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|11559441|dbj|BAB18800.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+QFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLV+LATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVLLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLSALGVNAVAYYRGLDVSVIPTSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKIFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPA+IPDREVLVREFDEMEEC
 Sbjct 1687 ILSGKPAVIPDREVLVREFDEMEEC 1711

> gi|56342185|dbj|BAD73970.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
 Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg 120
 T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG
 Sbjct 1087 TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DSRGSLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFETDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
 SPVFETDSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA
 Sbjct 1207 SPVFETDSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNVGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHS+KKCDELAALK +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSRKKCDELAALKSSLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTQKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMCMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVIVGRI 1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPAIIPDREVLV++FDEMEEC
 Sbjct 1687 ILSGKPAIIPDREVLVQQFDEMEEC 1711

> gi|7650254|gb|AAF65958.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL+GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLIGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAQPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGINAVAYYRGLDVSVIPTSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQA PPSWDMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQALPPSWDMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

>gi|5918933|gb|AAD56182.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPN+RTGVRTITTTG+ ITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGASITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELATKLSTLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETATVPQDAVSRQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYREFDEMEEC 1711	

>gi|1814088|dbj|BAA09074.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCG SDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSV ATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHS D+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLP CQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GENLPYLVAIQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQN++TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAAL AYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLRYEFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDRE LY+EFDEMEEC 1711	

> [gi|1160328|dbj|BAA03375.1](#) polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPN+RTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNVRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYD+GCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDSGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAIQATVCAR+QAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARSQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PA+IPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLRYREFDEMEEC 1711	

> [gi|56342203|dbj|BAD73979.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLKGS SGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKGS SGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQQFDEMEEC 1711	

> gi|56342189|dbj|BAD73972.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTIETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTQK+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC 1711	

> gi|7650252|gb|AAF65957.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGSSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSSGGPLLCPPLGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTIETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTIETTTVPQDAVSRSQRRGRTGRGRIGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTP+ETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPSETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTGSVIVIGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC	1711

> [gi|7650242|gb|AAF65952.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKGS SGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETT+R	
Sbjct	1147	DSRGSLLSPRPVSYLKGS SGGPLLCPSGHIVGIFRAAVCTRGVAKAVDFIPVESMETTIR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVR ITTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRAITTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL +LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSSSLG LNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTRG+ G+YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTRGRMGVYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600

Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PA++PDREVLRY++FDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLRYQQFDEMEEC 1711	

> gi|5918959|gb|AAD56195.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRP+SYLKSSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DGRGSLSPRPVSYLKSSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGIRITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA+IPDREVLRY+EFDEMEEC
 Sbjct 1687 ILSGKPAVIPDREVLRYQEFDEMEEC 1711

> gi|5918943|gb|AAD56187.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHGAG 1086

Query 61 TRTIASPKGPVIMQYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE +ETTMR
 Sbjct 1147 DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVEAMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG +PNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGTEPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK 1386

Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKLSALGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSG+PA+IPDREVLRYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLRYREFDEMEEC 1711

> gi|27544244|dbj|BAC54896.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKGS SGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKGS SGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET++RLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSIRLRLAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC	1711

> gi|11559453|dbj|BAB18806.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDREVLY+EFDEMEEC 1711	

> gi|56342243|dbj|BAD73999.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPO+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLŠGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|56342241|dbj|BAD73998.1 polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCELAALKSLGLLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC 1711	

>gi|56342237|dbj|BAD73996.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	

Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHS+KKCDELAALKL LG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLGLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 +LSGKPAI+PDREVL Y+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVL YQEFDEMEEC 1711	

>gi|11559461|dbj|BAB18810.1| polyprotein [Hepatitis C virus]
Length=3014

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSGGPLLCPLGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS+TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSSTGEIPFYGKAIPLEVIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPA+IPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLRYREFDEMEEC 1711	

>gi|221615|dbj|BAA18894.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYXQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWHAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAA GYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAAGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTG PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTGGPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLV YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVVYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTGTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLRYREFDEMEEC 1711	

>gi|56342239|dbj|BAD73997.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3167), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKGS SGGPLLC P+GAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGS SGGPLLC PSHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELA AKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSRKKCDELA AKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC	1711

> gi|1814085|dbj|BAA09071.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3167), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCG SDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSV ATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVTATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHS D+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSIDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSLGLNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRGTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRGTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLP CQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPFCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GENLPYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENLPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAAL AYCL+TG VVIVGR+	

Sbjct 1627 RLGAVQNDVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALTAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPA+IPDRE LY+EFDEMEEC

Sbjct 1687 ILSGKPAVIPDREALYQEFDEMEEC 1711

>gi|56342201|dbj|BAD73978.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG

Sbjct 1027 APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
DSRGILLSPRP+SYLGSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR

Sbjct 1147 DSRGILLSPRPVSYLGSSGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 300
YMSKAHGIDPNIRTGVRTITTG+PITYSTYKGFLADGGCGSGGAYDIIICDECHSTD+T+I

Sbjct 1267 YMSKAHGIDPNIRTGVRTITTGAPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
GGRHLIFCHS+KKCDELAACKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSRKKCDELAACKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE 480
DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE

Sbjct 1447 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
HIDAFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY

Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
RLGAVQNE+TLTHP+TK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVTLTHPITKFITACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPA+IPDREVLRY++FDEMEEC

Sbjct 1687 ILSGKPAVIPDREVLRYQQFDEMEEC 1711

> gi|7650264|gb|AAF65963.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG+LGCIIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGVLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+ ITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGASITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPFYGKAIPLENIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRL+PTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDMWKCLIRLRPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPVVDPDREVLRYREFDEMEEC	1711

> gi|5918941|gb|AAD56186.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE +ETTMR DTRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG +PNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGTEPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL ALG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG GGRHLIFCHSKKKKCELA AAKLSALGLNAVAYYRGLDVSVIP TSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPITKFIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSG+PA+IPDREVLYREFDEMEEC ILSGRPAVIPDREVLYREFDEMEEC	1711

> [gi|5441842|emb|CAB46917.1|](#) non-structural polyprotein [Hepatitis C virus]
[gi|5441836|emb|CAB46913.1|](#) non-structural polyprotein [Hepatitis C virus]
 Length=1985

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	2	APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	61

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	62	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	121
Query	121	dsrgsllsprPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGP LLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	122	DSRGSLLSPRPVS YLGSSGGP LLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	181
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	182	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	241
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	242	YMSKAHGIDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	301
Query	301	LGIGTVLDQAE TAGARLVVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE TAGARLVVLATATPPG SVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	
Sbjct	302	LGIGTVLDQAE TAGARLVVLATATPPG SVTVPHPNIEEVALSSTTGEIPFYGKAIPETIK	361
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	362	GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIP TSGDVIVVATDALMTGFTG	421
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	422	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIYRFVTPGE	481
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	482	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	541
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	542	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	601
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVV TSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	602	RLGAVQNEVTTTHPITKYIMACMSADLEVV TSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	661
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPAIIPDREVL YREFDEMEEC	
Sbjct	662	ILSGKPAIIPDREVL YREFDEMEEC 686	

> gi|56342193|dbj|BAD73974.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1223 bits (3165), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCI VTS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		RT+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	ARTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGP LLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	

Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSCGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSCGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS +GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|11559459|dbj|BAB18809.1 polyprotein [Hepatitis C virus]
Length=3010

Score = 1223 bits (3165), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRPISYLGSSGGPLLC GH VGIFRAAVCTRGVAKAV+F+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPN+RTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G++ PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSG+PAIIPDREVLY+EFDEMEEC 1711	

> [gi|56342191|dbj|BAD73973.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrrg	120
Sbjct	1087	T+T+A GP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC 1711	

> [gi|7650224|gb|AAF65943.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA QTFLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQTFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTI+T T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIDTTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		IDAHFLSQTKQ+G+N PY+VAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	RIDAHFLSQTKQAGDNFPYMVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC	685
		+LSG+PAIIPDREVL YREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVL YREFDEMEEC	1711

>gi|11559465|dbj|BAB18812.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1148	DGRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1207
Query	181	SPVF TDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATL FGA	
Sbjct	1208	SPVF TDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLSFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1268	YMSKAHGTDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIP+E IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPFYGKAIPIEAIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIP TNGDVVVVATDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTTVPQDAVSR+QRRGRTGRGRRGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET++RLRAY+NTPGLPVCQDHLEFWEGVFTGLT	

Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSIRLRLAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI LTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEIILTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1688	ILSGRPAVVPDREVLRYREFDEMEEC 1712	

>gi|11559443|dbj|BAB18801.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLA+C+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLASCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKGS SGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLKGS SGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LGINA+AYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGINAIAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAV NE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVHNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSG+PA+IPDREVLYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLYREFDEMEEC 1711

> gi|56342229|dbj|BAD73992.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
 T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG
 Sbjct 1087 TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSRLTPCTCGSSDLYLVRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAYGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSRKKCDELAALKSLGLNNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVDfSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDfSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVDfSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+URLRAY+NTPLPVCQDHLEFWEGVFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSURLRAYLNTPLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPAI+PDREVLY+EFDEMEEC

Sbjct 1687 ILSGKPAILPDREVLYQEFDEMEEC 1711

> gi|56342225|dbj|BAD73990.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		+GIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	MGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLLNAVAYYRGLDVSVIP TNGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMCMSADLEVATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQQFDEMEEC 1711	

> gi|56342199|dbj|BAD73977.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFOVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FOVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLFEWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC 1711	

>gi|56342197|dbj|BAD73976.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086

Query	61	TRTIASPKGPFVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKKCELA AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|56342195|dbj|BAD73975.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPFVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	RT+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS +GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNSGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLSDLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC 1711	

> gi|496367|dbj|BAA03905.1| polyprotein precursor [Hepatitis C virus type 2]
Length=2284

Score = 1222 bits (3162), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	301	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAG	360
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSPTCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	361	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	420
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VGI FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	421	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	480
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLNPSVAATLGFGA	240
Sbjct	481	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVRVLNPSVAATLGFGA	540

Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	541	YMSKAHGI+PNIRTGVRTITTG PITYSTYKFLADGGCSGGAYDIIICDECHSTD T+I	600
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	601	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	660
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	661	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	720
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	721	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	780
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
Sbjct	781	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLFEW VFTGLT	840
Query	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	841	HIDAHFLSQTKQ+G+N PYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	900
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	901	RLGAVQNEITLTHP+TK++M CMSADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+	960
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	961	+LSG+PA++PDREVLYREFDEMEEC	985

> [gi|1749762|dbj|BAA14035.1](#) unnamed protein product [Hepatitis C virus]
Length=3010

Score = 1222 bits (3162), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYK VLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGI+PNIRTGVRTITTG PITYSTYKFLADGGCSGGAYDIIICDECHSTD T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TK++M CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKFVMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRAVVPDREVLYREFDEMEEC 1711	

> [gi|56342227|dbj|BAD73991.1|](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK +GIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	MGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNVGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHS+KKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSRKKCDELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggv laalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC	1711

> [gi|7650226|gb|AAF65944.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 660/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTVYHGAG	
Sbjct	1027	APITAYSQQTRGMLGCIITS LTGRDKNQVEGEVQVSTATQSF LATCVNGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQV HLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVGH LHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAE TAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE TAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAE TAGARLVVLATATPPGSVTVPHPNIEEAALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|56342209|dbj|BAD73982.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1221 bits (3160), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DP+IRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPSIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVATDALMTGYTG GGRHLIFCHS+KKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSRKKCELAALKLSSGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTITETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLDPFTTITET T+PQDAVSR+QRRGRTRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTITETTTVPQDAVSRSQRRGRTRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

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Query 601  RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
           RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct 1627 RLGAVQNEVTLTHPITKIFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661  VLSGKPAIIPDREVLYREFDEMEEC 685
           +LSGKPA++PDREVLY++FDEMEEC
Sbjct 1687 ILSGKPAVLPDREVLYQQFDEMEEC 1711

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> gi|5918935|gb|AAD56183.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3160), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

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Query 1  APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
Sbjct 1027 APITAYSQQTRGLFGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61  TRTIASPKGPVIMQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
           ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
           DSRGSLSPRP+SYLGSSGGPLLC+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
Sbjct 1147 DSRGSLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
           SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTVGRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
           YMSKAHGIDPN+RTGVRTITTG+ ITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI
Sbjct 1267 YMSKAHGIDPNVRTGVRTITTGASITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
           LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK
Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
           GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG
Sbjct 1387 GGRHLIFCHSKKKCDELATKLSTLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG 1446

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
           DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
Sbjct 1447 DFDSVIDCNTCVTQTVD FSLDPTFTIETATVPQDAVSRQRRGRTGRGRMG IYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
           RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
           HIDAFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQM KCLIRLKP TLHGPTPLLY
Sbjct 1567 HIDAFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMLKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
           RLGAVQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct 1627 RLGAVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685

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+LSG+PAIIPDREVLVREFDEMEEC
 Sbjct 1687 ILSGRPAIIPDREVLVREFDEMEEC 1711

> gi|56342215|dbj|BAD73985.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSL PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLIPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+ G VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTAGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSGKPAI+PDREVLV++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLVQQFDEMEEC 1711	

> gi|56342211|dbj|BAD73983.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPISIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSSGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAVLPDREVLYQQFDEMEEC 1711	

> [gi|7650238|gb|AAF65950.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg +T+A PKGP+ QMYTNVDQDLVGW +P G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	AKTLAGPKGPITQMYTNVDQDLVGWQSPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGI+P+IRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIEPSIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LG+GTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGVGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSGLGLNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGA+QNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGALQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|31980453|dbj|BAC77767.1 NS protein [Hepatitis C virus]
Length=1984

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	61	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	120

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKA P+E IK	360
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVT KYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	601	RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	661	+LSGKPA+IPDREVLY+EFDEMEEC 685	

> gi|1814086|dbj|BAA09072.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKS KVP YAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GSKSNKVPVEYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYTGKFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPV QDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDREVLYREFDEMEEC 1711	

> gi|56342231|dbj|BAD73993.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRTITTTG+PITYSTYTGKFLADGGCSGGAYDIIICDECHSTD+T+I	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685.	
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAILPDREVLYQEFDEMEEC 1711	

> [gi|7650230|gb|AAF65946.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T++	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	

Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRG+TGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGKTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPA+IPDREVL YREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVL YREFDEMEEC 1711	

> [gi|221611|dbj|BAA14233.1](#) unnamed protein product [Hepatitis C virus]
[gi|130469|sp|P26662|POLG_HCVJA](#) Genome polyprotein [Contains: Core protein p21 (Capsid C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSF LATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADV+PVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMT PCTCGSSDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGI+PNIRTGVRTITTTG PITYSTY KFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIEPNIRTGVRTITTTGGPITYSTYCKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAACL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKKCELAACL TGLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSR QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRAQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+NLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNLPLYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|1181832|gb|AAA86907.1| polyprotein
Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GK+TKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALS GEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSNIGEIPFYGKAIPLENIK	1386
Query	361	GGRHLIFCHSKKKKCELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHS+KKCELAACL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSRKKKCELAACL SGLGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCN CVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNVCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCE YDAGCAWYELTPAE +VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCE SYDAGCAWYELTPAEASVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKIFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIVPDREVLYQEFDEMEEC 1711	

> [gi|4753719|emb|CAB41950.1|](#) polyprotein [Hepatitis C virus]
 Length=3012

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1029	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLV+RHADVIPVRRRG	
Sbjct	1089	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVSRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETT R	
Sbjct	1149	DSRGSLSPRPVSYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVEMETTTR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1209	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1269	YMSKAHGVDPSIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1329	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIR	1388
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA A+L LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1389	GGRHLIFCHSKKKCDELA AQLSGLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTRG+ GIYRFV PGE	
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTRGRRGIYRFVTPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct	1569	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1629	RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1688
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDR VLYREFDEMEEC	
Sbjct	1689	ILSGKPAIVPDRGVLYREFDEMEEC 1713	

> gi|56342221|dbj|BAD73988.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DP+IRTGVRT+TTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVS+IP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCV QTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPAI+PDREVLV++FDEMEEC
 Sbjct 1687 ILSGKPAIVPDREVLVQQFDEMEEC 1711

>gi|56342217|dbj|BAD73986.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+AS KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLASQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG++PNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVEPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCE+AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCEVAALKSLGLNNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPV LHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ THP+TKYIMTCM+ADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVIFTHPITKYIMTCMAADLEVATSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSGKPAI+PDREVLV++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLVQQFDEMEEC 1711	

> gi|56342213|dbj|BAD73984.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSL PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLIPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD SLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDLSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+ G VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITK FIMACMSADLEVATSTWVLVGGVLAALAAAYCLTAGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	I LSGKPAIIPDREVLYQQFDEMEEC	1711

> gi|221605|dbj|BAA02756.1| polyprotein precursor [Hepatitis C virus]
Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGS SGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YM KAHGIDPNIRTGVRTITTTG PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL LG+NAVAYYRGLDVSVIPPIGDV VVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWE VFTGL+	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSGKPA++PDREVLY+EFDEMEEC	1711

> gi|1814087|dbj|BAA09073.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+ IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLDTIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGRHLIF HSKKKKCELA KL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFWHSKKKKCELATKLSALGVNAVAYYRGLDVSVIPTSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVIQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		R SGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RTSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> gi|18027685|gb|AAL55821.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCI VTS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVCTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVCTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|7650250|gb|AAF65956.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGP L LCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETT R	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	

Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLLNAVAYYRGLDVSVIPVSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		D DSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DLDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTQK+G+NLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQKAGDNLPLYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLYREFDEMEEC 1711	

> gi|11559467|dbj|BAB18813.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFATCINGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYA QGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYATQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPN+RTGVRT+TTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGMDPNLRTGVRTVTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		+FDSVIDCNTCV QTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	NFDSVIDCNTCVNQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQEFDEMEEC 1711	

> gi|11559463|dbj|BAB18811.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DS+GSLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSKGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAL+L++LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAARLLSLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWD MWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDLMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVVLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+P IIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPVIIPDREVLYREFDEMEEC 1711	

> [gi|56342205|dbj|BAD73980.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1219 bits (3154), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL GCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLFGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLT PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLT PCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGP LCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVS YLGSSGGP LCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDP+IRTGVRTIT TGG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPSIRTGVRTIT TGGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTV PHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV PHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV PHPNIEEVALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA KL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELA EKLSLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPVTKFITACMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQQFDEMEEC	1711

> [gi|385584|gb|AAB27127.1|](#) polyprotein [Hepatitis C virus]

[gi|743453|prf|12012309A](#) polyprotein

Length=3014

Score = 1218 bits (3152), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY++QTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQRTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPIAQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKGS SGGP L LCP+GHAVG+FRFAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPVS Y LKGS SGGP L LCPSGHAVGVFRFAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TD SSPP VPQ+FQVAHLHAPTGS GKST+VPAAYA QGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TD TSSPPAVPQT FQVAHLHAPTGS GKSTRVPAAYATQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT T GSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTIT T G+PITYSTY GKFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTIT T GAPITYSTY GKFLADGGCSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIM	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AAKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AAKLSGLGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQT VDFSLDPTFTIETITLPQDAVSrtqrrgrtg r gKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQT VDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQT VDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDS PVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660

Sbjct 1627 RLGAVQNE+TLTHP+TKYIM CM ADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+ 1686
 RLGAVQNEVTLTHPITKYIMACMWADLEVVSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI
 Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSG+PA++PDREVLVREFDEMEEC
 Sbjct 1687 ILSGRPAVVPDREVLVREFDEMEEC 1711

> gi|560789|dbj|BAA06303.1 polyprotein [Hepatitis C virus]
 Length=3010

Score = 1218 bits (3151), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHHGAG 1086
 Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPV RRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGSAPPGARSLTPCTCGSSDLVLRHADVIPVHRRG 1146
 Query 121 dsrgsllsprPISYLKSSSGGPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSP PISYLKSSSGGPL CP+G VGIFRAAVCTRGVAKAVDF+PVE++ETMR
 Sbjct 1147 DSRGSLSPGPISYLKSSSGGPLPCPSGRVVGIFRAAVCTRGVAKAVDFVPVESMETMR 1206
 Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGST+VPAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTRVPAAYAAQGYKVLVNLNPSVAATLGFGA 1266
 Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI
 Sbjct 1267 YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI 1326
 Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK 1386
 Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVS+IP GDVVVVATDALMTGYTG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGYTG 1446
 Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE 1506
 Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566
 Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAQATVCARA+APPPSWDMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAQATVCARAKAPPPSWDMWKCLIRLKP TLHGPTPLLY 1626
 Query 601 RLGAVQNEITLTHPVTKYIMTMSADLEVVSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVVSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686
 Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSG+PA+IPDREVLV+EFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLVQEFDEMEEC 1711

> gi|56342219|dbj|BAD73987.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP V PQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG++PNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVEPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAAKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaayCLSTGCVVIVGRV	660
		RLGAVQNE+ THP+TK+IMTCM+ADLEV TSTWVLVGGVLAALAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVIFTHPITKFIMTCMAADLEVATSTWVLVGGVLAALAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	IISGKPAIIPDREVLYQQFDEMEEC	1711

> gi|3098633|gb|AAC15722.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.

Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLCIIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLVLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDV VVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGLNAVAYYRGLDVSVIPPIGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVVLGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVVLGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC	1711

> gi|86372255|gb|ABC95195.1| polyprotein [Hepatitis C virus]
 Length=3014

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1031	APITAYAQQTRGLLGCIIVTSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1090

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLT CTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1091	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTACTCGSSDLYLVTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+S LKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1151	DSRGSLSPRPLSNLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1210
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPV+TDNSSPP VPQ+FQVA+LHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1211	SPVYTDNSSPPAVPQTFQVAYLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1271	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1390
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHL FCHSKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1391	GGRHLTFCHSKKKCELAALKSSLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1451	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggylaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVI GR+	
Sbjct	1631	RLGAVQNEVTLTHPMTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGGSVVIAGRI	1690
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1691	ILSGRPAVVPDREVLYREFDEMEEC 1715	

> gi|67773303|gb|AA81920.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	

Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSCGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYTGKFLADGGCSCGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYTGKFLADGGCSCGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPGDV+VVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAACKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTTHPITKYIMACMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYREFDEMEEC 1711	

> [gi|56342223|dbj|BAD73989.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+P E +ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPAEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ++QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQAYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRT+TTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCV QTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> [gi|221607|dbj|BAA01583.1](#) polyprotein precursor [Hepatitis C virus]
Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIPPIGDIVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDIVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSGKPA++PDREVLV+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLVQEFDEMEEC 1711	

> gi|80322852|gb|ABB52628.1| polyprotein [Hepatitis C virus]
 Length=2314

Score = 1216 bits (3147), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	354	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	413
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTLPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	414	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSSTLPCTCGSSDLYLVTRHADVIPVRRRG	473
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLKSSGGPPLCP+GH GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	474	DNRGSLLSPRPISYLKSSGGPPLCPSGHVAGIFRAAVCTRGVAKAVDFVPVESMETTMR	533
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTK PAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	534	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKAPAAAYAAQGYKVLVLNPSVAATLGFGA	593
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDEC TD+TSI	
Sbjct	594	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECRPTDSTSI	653
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E K	
Sbjct	654	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETTK	713
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGR+LIFCHSKKKCDELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	714	GGRYLIFCHSKKKCDELAALKLSALGINAVAYYRGLDVSVIPTSGDIVVVVATDALMTGYTG	773

Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	774	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	833
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	834	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	893
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCL+RLKP TLHGPTPLLY	
Sbjct	894	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLMRLKP TLHGPTPLLY	953
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	954	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1013
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA IPDREVLYREFDEMEEC	
Sbjct	1014	IILSGRPATIPDREVLYREFDEMEEC	1038

>gi|5918963|gb|AAD56197.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3146), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYG+AIIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGRAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GRHLIFCHSKKKCELAALKL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	EGRHLIFCHSKKKCELAALKLSALGLNAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHP+TK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNDVTLTHPITKLIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRL	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

>gi|5918961|gb|AAD56196.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3146), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYG+AIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGRAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GRHLIFCHSKKKCDELAACKL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	EGRHLIFCHSKKKCDELAACKLSALGLNAVAYYRGLDVSVIP TSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626

Query 601 RLGA VQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV 660
 RLGA VQN++TLTHP+TK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGA VQNDVTLTHPITKLIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRL 1686

Query 661 VLSGKPAIIPDREVL YREFDEMEEC 685
 +LSG+PA+IPDREVL YREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVL YREFDEMEEC 1711

> [gi|1944376|dbj|BAA19625.1](#) unnamed protein product [Hepatitis C virus]
 Length=3010

Score = 1216 bits (3145), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLGSSGGPL CP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR
 Sbjct 1147 DSRGSLSPRPVS YLGSSGGPLPCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAA YAAQGYKVLVLNPSVAATLGFGA 240
 +PVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAA YAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 APVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAA YAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDII+CDECHSTD+T+I
 Sbjct 1267 YMSKAYGTDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIMCDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGT LDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 1327 LGIGTALDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK 1386

Query 361 GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELA AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKCELA AAKLSTLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPSWDQMWKCLIRL KPTLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQA PPSWDQMWKCL RLKPTLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQASPPSWDQMWKCLRLKPTLHGPTPLLY 1626

Query 601 RLGA VQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV 660
 RLGA VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGA VQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVL YREFDEMEEC 685
 +LSGKPA+IPDREVL YREFDEMEEC

Sbjct 1687 ILSGKPAVIPDREVLRYREFDEMEEC 1711

> gi|1814089|dbj|BAA09076.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3145), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 657/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCTNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGSKGPITQMYTNVDQDLVGWQAPSGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSK KVP YAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSKNKPVEYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKSLGLGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPV QDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVPVQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlyvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLYVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMCMSADLEVVTSTWVLYVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLRYREFDEMEEC 1711	

> gi|19568933|gb|AAL91977.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC++G CWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG++PNIRTGVRT+TTG+ ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTRGR+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VR+RAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	R+GAVQNE+ LTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDRE LY+ FDEMEEC 1711	

>gi|56342235|dbj|BAD73995.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVS YLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCN CVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTRGR+ G YRFV PGE DFDSVIDCNVCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTRGRGTGT YRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVVLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDRE LY++FDEMEEC ILSGKPAIVPDREALYQQFDEMEEC 1711	

> gi|56342233|dbj|BAD73994.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCN CVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	480
Sbjct	1447	DFDSVIDCNVCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGTYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVVLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDRE LY++FDEMEEC	
Sbjct	1687	IILSGKPAIVPDREALYQQFDEMEEC 1711	

>gi|3098637|gb|AAC15724.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRG+LGC+ITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGVLCVITS LTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDL DLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDIVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAW+ELTPAET+VRLRAY+NTPGLPVCQDHLFEW VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA++PDREVLY+EFDEMEEC 1711	

> [gi|15487694|gb|AAL00900.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1214 bits (3142), Expect = 0.0, Method: Composition-based stats.
 Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFG	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T++	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAACL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAACL SGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE D DSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DSDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSR SQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTQK+G+N PYLVA YQATVCARAQAPPPSWDMWK LIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKS LIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLG VQ+EITLTHPVTKYIM CMSADLEVVTSTWVLV GVLAAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGTQVQSEITLTHPVTKYIMACMSADLEVVTSTWVLVSGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> [gi|3098635|gb|AAC15723.1|](#) polyprotein [Hepatitis C virus]

Length=3010

Score = 1214 bits (3141), Expect = 0.0, Method: Composition-based stats.
Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRG+LGC+ITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGVLCVITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+ QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTSQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGGSITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAACL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAACL TGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWV VGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVPVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC	1711

> gi|3098651|gb|AAC15730.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1214 bits (3140), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVGLGCVITSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS\RLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|3098648|gb|AAC15729.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1213 bits (3139), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYSQQTRGV LGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGS SGGP L LCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETMR DSRGSLLSPRPVSYLKGS SGGP L LCPSGHVGVFRAAVCTRGVAKAVDFIPVESMETMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNS+PP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSTPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGIDPNIRTGVRTITTTGGSITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG GGRHLIFCHSKKKCDELA AKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGR TG RG+ GIYRFV PGE DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGR TG RGSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS\RLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626

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Query   601   RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV   660
          RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   1627   RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI   1686

Query   661   VLSGKPAIIPDREVLYREFDEMEEC   685
          +LSGKPA++PDREVLY+EFDEMEEC
Sbjct   1687   ILSGKPAVVPDREVLYQEFDMEEC   1711

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> gi|15529111|gb|AAK97744.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

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Query    1   APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60
          APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG
Sbjct   1027   APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGACWTVFHGAG   1086

Query    61   TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg   120
          ++T+A PKGP+ QMYTNVD DLVGW AP GRSSTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   1087   SKTLAGPKGPITQMYTNVDLDLVGWQAPPGSRSSTPCTCGSSDLYLVTRHADVIPVRRRG   1146

Query   121   dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR   180
          DSRGSLSPRP+SYLGSSGGPLLCP+ HAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR
Sbjct   1147   DSRGSLSPRPVSYLGSSGGPLLCPSRHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR   1206

Query   181   SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240
          SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   1207   SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   1266

Query   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI   300
          YMSKAHGIDPNIRTGVR ITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I
Sbjct   1267   YMSKAHGIDPNIRTGVRAITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI   1326

Query   301   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK   360
          LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+EVIK
Sbjct   1327   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEIPFYGKAIPLEVIK   1386

Query   361   GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG   420
          GGRHLIFCHSKKK DELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   1387   GGRHLIFCHSKKKYDELAALKLSALGLNAVAYYRGLDVSVIP TNGDVVVVATDALMTGFTG   1446

Query   421   DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE   480
          DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAV+R+QRRGRTGRG+ GIYRFV PGE
Sbjct   1447   DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVARSQRRGRTGRGRRGIYRFVTPGE   1506

Query   481   RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT   540
          RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPPLPVCQDHLEFWE V TGLT
Sbjct   1507   RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVSTGLT   1566

Query   541   HIDAHLFSQTKQSGENLPYLVAIQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY   600
          HIDAHLFSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY
Sbjct   1567   HIDAHLFSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY   1626

Query   601   RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV   660
          RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   1627   RLGAVQNEITLTHPMTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI   1686

Query   661   VLSGKPAIIPDREVLYREFDEMEEC   685

```

+LSG+PA+IPDREVLYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLYREFDEMEEC 1711

> gi|3098644|gb|AAC15727.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
 Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIIITSLSLGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVGLGCIITSLSLGRDKNQVEGEVQVVSTATHSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV+PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRTGRGRSGIYRFVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|3098639|gb|AAC15725.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC ITS LTGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGXCITS LTGRDKNQVEGEVQVVSTATXSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSSGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSSGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSSGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG IYTYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

>gi|1814090|dbj|BAA09075.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1212 bits (3136), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFDTNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFDTNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFDTNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTG RTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+ IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLDTIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIF HSKKKCDELA KL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFWHSKKKCDELATKLSALGVNAVAYYRGLDVSVIPTSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCV QT DFSLDPFTTETIET.T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVIQTDDFSLDPFTTETIETRTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEVFTGLT R SGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RTSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV RLGAVQNE+ LTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVILTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSGKPA+IPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLRYREFDEMEEC 1711	

> [gi|56342207|dbj|BAD73981.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1212 bits (3135), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 657/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTR+ADVIPVRRRG	120
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRYADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPGLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPGLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTM	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPGLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA KL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAVKLSSLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+Q RGRTG G G+YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQLRGRTGSGTTGMYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		R SGMFDSSVLCECYDAGC WYELTPAET+VRLRAY+N PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RTSGMFDSSVLCECYDAGCTWYELTPAETSVRLRAYLNAPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		IDAHF+SQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	KIDAHFMSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAI+PDREVLY++FDEMEEC	
Sbjct	1687	IILSGRPAIVPDREVLYQQFDEMEEC 1711	

>gi|3098646|gb|AAC15728.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1212 bits (3135), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCVITSLSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPGLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPGLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTM	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPGLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVFLDPTFTIETITLPPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVFLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAW+ELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA++PDREVLY+EFDEMEEC 1711	

> [gi|59479|emb|CAA43793.1|](#) JK1-full [Hepatitis C virus]
Length=3010

Score = 1211 bits (3134), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 658/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGL GCI+TSLTGRDKNQVEGE Q+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+ SLTPCT GSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNI TGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLA ATPPGSVTVPHPNIEEVAL TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLAATPPGSVTVPHPNIEEVALPNTGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPA T+VRLRAY+NTPGLPVCQ HLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAVTSVRLRAYLNTPLPVCQVHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

> gi|3810874|dbj|BAA20975.1| precursor polyprotein [Hepatitis C virus]
Length=1186

Score = 1211 bits (3134), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	
Sbjct	305	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAG	364
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	365	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	424
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	425	DSRGSLSPRPVSYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	484
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	485	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	544
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGI+PNIRTGVRTITTTG PITYSTY KFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	545	YMSKAHGIEPNIRTGVRTITTTGGPITYSTYCKFLADGGCSGGAYDIIICDECHSTDSTTI	604
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	605	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	664
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL LG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG	

Sbjct	665	GGRHLIFCHSKKKCDELAACKLTGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	724
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSR QRRGRTGRG+ GIYRFV PGE	
Sbjct	725	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRAQRRGRTGRGRSGIYRFVTPGE	784
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLFEW VFTGLT	
Sbjct	785	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLFEWESVFTGLT	844
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	845	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	904
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK++M CMSADLEVVSTWVlvvggvlalaaYCL+TG VVIVGR+	
Sbjct	905	RLGAVQNEITLTHPITKFVMACMSADLEVVSTWVlvvggvlalaaYCLTTGSVVIVGRI	964
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEME C	
Sbjct	965	ILSGRPVAVPDREVLYREFDEMEAC 989	

> gi|3098653|gb|AAC15731.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1211 bits (3132), Expect = 0.0, Method: Composition-based stats.
 Identities = 621/685 (90%), Positives = 660/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		A ITAY+QQTRG+LGC+ITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	ASITAYSQQTRGVLGCVITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLSLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAACKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPA++PDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLRYQEFDEMEEC 1711	

> gi|3098642|gb|AAC15726.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1210 bits (3131), Expect = 0.0, Method: Composition-based stats.
 Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCVITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+ QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTSQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	

Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWV VGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVPVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA++PDREVLRY+EFDEMEEC

Sbjct 1687 ILSGKPAVVPDREVLRYQEFDEMEEC 1711

> gi|3098655|gb|AAC15732.1| polyprotein [Hepatitis C virus]

Length=2864

Score = 1210 bits (3130), Expect = 0.0, Method: Composition-based stats.

Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APIT Y+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG

Sbjct 1027 APITTYSQQTRGVLGCIITSLTGRDKNQVEGEVQVVSTATHSFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 SKTLAGPKGPITQMYTNVDLVLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR

Sbjct 1147 DSRGSLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQV HLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQTFQVHHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I

Sbjct 1267 YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDfSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDfSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV+PGE

Sbjct 1447 DFDSVIDCNTCVTQTVDfSLDPTFTIETTTVPQDAVSRQRRGRTGRGRSGIYRFVSPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAFLSQTQKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAFLSQTQKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY

Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA++PDREVLRY+EFDEMEEC
 Sbjct 1687 ILSGKPAVVPDREVLRYQEFDEMEEC 1711

> gi|80322850|gb|ABB52627.1| polyprotein [Hepatitis C virus]
 Length=2383

Score = 1209 bits (3127), Expect = 0.0, Method: Composition-based stats.
 Identities = 620/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 423 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 482

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+IQMYTNVDQDLVGW AP G+RSLTPCTCGSSD YLVTRHADVIPVRRRG
 Sbjct 483 SKTLAGPKGPIIQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDPYLVTRHADVIPVRRRG 542

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D RGSLLSP+PISYLGSSGGPLLCP+GHAVGIFRAAVCTRG+AKAVDF+P E +ETTMR
 Sbjct 543 DGRGSLLSPKPIISYLGSSGGPLLCPSGHAVGIFRAAVCTRGIAKAVDFVPAECMETTMR 602

Query 181 SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
 SPVFTD+SSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLPSVAATL FGA
 Sbjct 603 SPVFTDHSSPPTVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLPSVAATLSFGA 662

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTG+RTITTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T++
 Sbjct 663 YMSKAHGVDPNIRTGMRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTV 722

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 723 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK 782

Query 361 GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELAACKL LG+NAV YYRGLDVSVIP GDVVVVATDALMTGYTG
 Sbjct 783 GGRHLIFCHSKKKCDELAACKLSGLGLNAVYRGLDVSVIPTSGDVVVVATDALMTGYTG 842

Query 421 DFDSVIDCNCVQTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
 DFDSVIDCNCVQTQTVDFSLDPTFTI+T T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 843 DFDSVIDCNCVQTQTVDFSLDPTFTIDTTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE 902

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 903 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT 962

Query 541 HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAH LSQTK +G+N PYLVAYQATVCARAQAPPPSWDQMWKCL+RLKP TLHGPTPLLY
 Sbjct 963 HIDAHLLSQTKDAGDNYPYLVAYQATVCARAQAPPPSWDQMWKCLMRLKP TLHGPTPLLY 1022

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggylaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TKYI+TCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1023 RLGAVQNEVTLTHPITKYIITCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1082

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA+IPDREVLRY+ FDEMEEC
 Sbjct 1083 ILSGKPAVIPDREVLRYQAFDEMEEC 1107

> gi|2943784|dbj|BAA25076.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1207 bits (3123), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 658/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTAKQSFLATCVNGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++T+A+ KGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	SKTLAAAKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGY VLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYMVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAET GAR VVLATATPPGS+T PHPNIEEV L+ TGEIPFY K IP+EVI+	
Sbjct	1327	LGIGTVLDQAETVGARFVVLATATPPGSITFPHPNIEEVPLANTGEIPFYAKTIPIEVIR	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPS MFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSAMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA+APPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAKAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> [gi|81960062|sp|Q913D4|POLG_HCVIN](#) Genome polyprotein [Contains: Core protein p21 (C; C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)].

gi|15422183|gb|AAK95832.1| polyprotein [Hepatitis C virus (isolate India)]
Length=3011

Score = 1207 bits (3123), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 651/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGE+QIVSTA QTFLATCING CWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEIQIVSTATQTFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+RTIAS GPV++MYTNVDQDLVGWPAPQG+RSLTPCTCG+SDLYLVTRHADVIPVRRRG	
Sbjct	1087	SRTIASASGPVVRMYTNVDQDLVGWPAPQGARSLTPCTCGASDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLCP GH GIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLCPMGHVAGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPTVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTTGSPITYSTYKGFLADGGC GGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGSPITYSTYKGFLADGGCPGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL VLATATPPG VTVPH NIEEVALS GE PFYGKAIP L IK	
Sbjct	1327	LGIGTVLDQAETAGVRLTVLATATPPGLVTVPHSNIEEVALSADGEKPFYGKAIP LNYIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKV LG+NAVA+YRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKVGLGVNAVAFYRGLDVSVIPPTTGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITLPQDAVSrtgrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVDFSLDP F+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	
Sbjct	1447	DFDSVIDCNTCVVQTVDFSLDPIFSIETSTVPQDAVSRSQRRGRTGRGKHGIYRYVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARA+APPPSWDQMWKCLIRLKPTL G TPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARARAPPPSWDQMWKCLIRLKPTLTGATPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLG+VQNEITLTHP+T+YIM CMSADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	
Sbjct	1627	RLGSVQNEITLTHPITQYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+L GKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILGGKPAVIPDREVLYREFDEMEEC 1711	

> gi|38492205|gb|AAR22408.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1204 bits (3114), Expect = 0.0, Method: Composition-based stats.
Identities = 616/685 (89%), Positives = 653/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGS SGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG +PNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQA+T GARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrrgtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+P RGRTRGR+ G YRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE++LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	LSG+PA+IPDREVLY+EFDEMEEC	1711

> gi|306287|gb|AAA45721.1| putative
Length=3010

Score = 1199 bits (3102), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgslspsrPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLL PRP+SYLKSSGGPLLCP+GHAVGI AAVCTRGVA AV+FIPVE++ETTMR	
Sbjct	1147	DGRGSLPPRPVSYLKSSGGPLLCPSGHAVGILPAAVCTRGVAMAVEFIPVESMETTMR	1206
Query	181	SPVFNDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFNDN SPP VPQ+FQVAHLHAPTGSKGST+VPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFNDNPSPPAVPQTFQVAHLHAPTGSKGSTRVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTTG+PITYSTYKGFLADGG SGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNLRTGVRTITTTGAPITYSTYKGFLADGGSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		GIGTVLDQAETAGARLVVL+TATPPGSVTVPH NIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	YGIGTVLDQAETAGARLVVLSTATPPGSVTVPHLNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEF EGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFSEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWD+MW+CLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAQATVCARAQAPPPSWDEMMWRCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMTMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC	1711

> gi|50235322|gb|AAT69968.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1199 bits (3101), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 648/685 (94%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLSLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIAS KGPVI MYTNVDQDL GW APQ SLTP +CGSSDLYLVRHADVIPV RRG	
Sbjct	1087	TRTIASSKGPVILMYTNVDQDLGGWTAPQVLGSLTPWSCGSSDLYLVRHADVIPVPRRG	1146
Query	121	dsrgslspsrPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		++RGSLLSPRPISYLKSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	ETRGSLSPRPISYLKSSGGPLLCPMGHAVGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSP VPQS+QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPLTVPQSYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGC GGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCPGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL VLATATPPGSVTVPH NIEEVALS GEIPFYGKAIP L IK	
Sbjct	1327	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHSNIEEVALSADGEIPFYGKAIP LNYIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKV G+NAVA+YRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVGPGVNAVAFYRGLDVSVIPPTTGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTITETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVD FSLDP F+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	
Sbjct	1447	DFDSVIDCNTCVVQTVD FSLDPIFSIETSTVPQDAVSRSQRRGRTGRGKHGIYRYVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARA+APPPSWDQMWKCLIRLKP TL G TPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYL VAYQATVCARARAPPPSWDQMWKCLIRLKP TLTGATPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLG+VQNEITLTHP+T+YIM CMSADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	
Sbjct	1627	RLGSVQNEITLTHPITQYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+L GKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILGGKPAVIPDREVLYREFDEMEEC 1711	

> [gi|567060|gb|AAA52748.1|](#) polyprotein
Length=3010

Score = 1198 bits (3100), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLL PRP+SYLKSSGGPLLCP+GHAVGI AAVCTRGVA AV+FIPVE++ETTMR	
Sbjct	1147	DGRGSLLPPRPVSYLKSSGGPLLCPSGHAVGILPAAVCTRGVAMAVEFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDN SPP VPQ+FQVAHLHAPTGSGBKST+VPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNPSPPAVPQTFQVAHLHAPTGSGBKSTRVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTTG+PITYSTYKGFLADGG SGGAYDII+CDECHSTD+T+I	

Sbjct	1267	YMSKAHGIDPNLRTGVRTITTTGAPITYSTYGKFLADGGGSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	GIGTVLDQAETAGARLVVL+TATPPGSVTVPH NIEEVALS TGEIPFYGKAIP+E IK YGIGTVLDQAETAGARLVVLSTATPPGSVTVPHLNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKCDELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLFEWGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLFEWGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GEN PYLVAAYQATVCARAQAPPPSWD+MW+CLIRLKP TLHGPTPLLY HIDAHFLSQTKQAGENFPYLVAAYQATVCARAQAPPPSWDEMWRCCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IMTCMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPITKFIIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDREVLY+EFDEMEEC ILSGKPAIIPDREVLYQEFDEMEEC 1711	

>gi|5748511|emb|CAB53095.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1197 bits (3098), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	A ITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG AHITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQMVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATL FGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSCGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRT TTTG+PITYSTYGKFLADGGCSCGGAYDIIICDECHSTD+T+I YMSKAHGIDPNIRTGVRTTTTGTGAPITYSTYGKFLADGGCSCGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGE+PFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEVPFYGKAIPETIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRIGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		VLSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC	1711

> gi|437108|gb|AAA75355.1| polyprotein
Length=3010

Score = 1197 bits (3098), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 652/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW A G RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAAPGMRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLL P+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLGSSGGPLLWPSPGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTG+PITYSTYGKF ADGGCGSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTGAPITYSTYGKFFADGGCGSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLD+AETAGARLVVLATATPPGS TVPHPNIEEVAL TGEIPFYG+AIP+E IK	
Sbjct	1327	LGIGTVLDRAETAGARLVVLATATPPGSTTVPHPNIEEVALPNTGEIPFYGRAIPIEFIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFC SKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCPSKKKKCELAALKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTFTIETTTVPQDAVSRTQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGL	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLN	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLI LKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIWLKPV LHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK IM MSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKLIMASMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|7650258|gb|AAF65960.1 polyprotein [Hepatitis C virus]
Length=3010

Score = 1195 bits (3092), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ Q+YTNVDQDL+GW AP GRSSTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQIYTNVDQDLGWQAPPGSRSSTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFOVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FOVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T++	
Sbjct	1267	YMSKAHGTDPNIRTGTRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVAL+ TGEIPFYGKAIP++VIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALTNTGEIPFYGKAIPIDVIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDS IDCNTCVTQTVDLSLDPFTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSXIDCNTCVTQTVDLSLDPFTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLG VQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGPVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC	1711

> [gi|4753721|emb|CAB41951.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1193 bits (3086), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLV+RHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVSRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH GIFRAAVCTRGVAKAVDF+PVE++ETT R	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVAGIFRAAVCTRGVAKAVDFVPVESMETTTR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTG RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPSIRTGTRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GG HLIFCHSKKKCDELAAL+L +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGGHLIFCHSKKKCDELAALSSLGVNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRGK GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGKRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	

Sbjct 1627 RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPAIIPDREVLRYREFDEMEEC

Sbjct 1687 ILSGKPAIIPDREVLRYREFDEMEEC 1711

> gi|7650262|gb|AAF65962.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1193 bits (3086), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG

Sbjct 1027 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
DSRGSLSPRPISYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR

Sbjct 1147 DSRGSLSPRPISYLGSSGGPLLCPSGHVVLGFRAAVCTRGVAKAVDFIPVEHMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGST+VPAAYAAQGYKVLVNLPSVAATL FGA

Sbjct 1207 SPVFTDNSSPPAVPQAFQVAHLHAPTGSKGSTRVPAAYAAQGYKVLVNLPSVAATLSFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
YMSKA+G+DPNIRTG RTITTG+ ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I

Sbjct 1267 YMSKAYGVDPNIRTGTRTITTGASITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGARLVVLATATPPGSVTVPHP+IEEVALS TGEIPFYGKAIP+EVIK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNTGEIPFYGKAIPIEVIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
GGRHLIFCHSKKKCDELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSKKKCDELAALKLSSLGMINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVQTQTVDFSLDPTFTTITITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
DFDSVIDCNCVQTQTVDFSLDPTFTT+T T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE

Sbjct 1447 DFDSVIDCNCVQTQTVDFSLDPTFTTIDTTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYEL PAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELAPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
HIDAHFLSQTKQ+G+N PYLVAQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQALPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSG+PA++PDREVLRYREFDEMEEC

Sbjct 1687 ILSGRPAVVPDREVLRYREFDEMEEC 1711

> gi|1405417|dbj|BAA09919.1| E1 and E2/NS1 envelope glycoprotein [Hepatitis C virus]
Length=3010

Score = 1191 bits (3080), Expect = 0.0, Method: Composition-based stats.
Identities = 614/685 (89%), Positives = 653/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQEVSTATQSFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTNRHADVIPVrrrg	120
		++ + PKGP+ QMYT+VDQDLVGW G+RSLTP TCGSS LYLVTNR+ADVIPVRR G	
Sbjct	1087	SKILVGPKGPITQMYTSVDQDLVGWVERPGARSLTPGTCGSSVLYLVTRNADVIPVRRGG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSP+P+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPKPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		S VFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SLVFTDNSSPPAVPQAFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSTLGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
		RP GMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPG VCQD+LEFWE VFTGLT	
Sbjct	1507	RPLGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPGFAVCQDYLEFWEDVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HI++HFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIESHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPVAVPDREVLYREFDEMEEC 1711	

> gi|67810846|gb|AA82011.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1174 bits (3037), Expect = 0.0, Method: Composition-based stats.
Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY	618
Sbjct	1627	RLGAVQNE+TLTHP+TKY	1644

> gi|67810857|gb|AA Y82016.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1172 bits (3033), Expect = 0.0, Method: Composition-based stats.
Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1149	DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+TLTHPVTKY	
Sbjct	1629	RLGAVQNEVTLTHPVTKY 1646	

> gi|67810849|gb|AA Y82012.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1172 bits (3032), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 612/618 (99%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DGRGSLLSPRPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMS+AHG+DPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQ+AVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQEAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

> gi|67810875|gb|AA82024.1| polyprotein [Hepatitis C virus]
gi|67810873|gb|AA82023.1| polyprotein [Hepatitis C virus]
 Length=1646

Score = 1171 bits (3030), Expect = 0.0, Method: Composition-based stats.
 Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTVGRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1269	YMSKAHGIDPNLRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1448

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYE TPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYEPTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTQKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1569	HIDAHFLSQTQKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1629	RLGAVQNEVTLTHPVTKY 1646	

> [gi|67810866|gb|AA82020.1|](#) polyprotein [Hepatitis C virus]
Length=1646

Score = 1171 bits (3029), Expect = 0.0, Method: Composition-based stats.
Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDEC STDATSI	
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECRSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTQKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	

Sbjct 1569 HIDAHLFSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1628

Query 601 RLGAVQNEITLTHPVTKY 618
RLGAVQNE+TLTHPVTKY

Sbjct 1629 RLGAVQNEVTLTHPVTKY 1646

> [gi|67810879|gb|AA82026.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG

Sbjct 1027 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 TRTIASPKGPVIQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
DSRGILLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR

Sbjct 1147 DSRGILLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR 1206

Query 181 SPVFTDNSSPPVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
SPVFTDNSSPP VPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI

Sbjct 1267 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALSTTGEIPFYGKAIPLE IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEALSTTGEIPFYGKAIPLEAIK 1386

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
GGRHLIFCHSKKKKCELAALKLVA+GINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG

Sbjct 1387 GGRHLIFCHSKKKKCELAALKLVAMGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG 1446

Query 421 DFDSVIDCNCVQTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgqgKPGIYRFVAPGE 480
DFDSVIDCNCVQTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE

Sbjct 1447 DFDSVIDCNCVQTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHLFSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
HIDAHLFSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 1567 HIDAHLFSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKY 618
RLGAVQNE+TLTHP+TKY

Sbjct 1627 RLGAVQNEVTLTHPITKY 1644

> [gi|67810877|gb|AA82025.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIT LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLV+GINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY 1644	

> [gi|67810842|gb|AA82009.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGS DLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDII+CDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHP+TKY	
Sbjct	1627	RLGAVQNEVTLTHPITKY 1644	

> gi|67810859|gb|AA82017.1| polyprotein [Hepatitis C virus]
 Length=1646

Score = 1170 bits (3026), Expect = 0.0, Method: Composition-based stats.
 Identities = 606/618 (98%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1149	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFI PVE+LETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300

Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1329	LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1388
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1629	RLGAVQNE+TLTHPVTKY 1646	

> gi|67810855|gb|AA82015.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1169 bits (3023), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DGRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLAALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

> [gi|67810853|gb|AAY82014.1|](#) polyprotein [Hepatitis C virus]
 Length=1644

Score = 1169 bits (3023), Expect = 0.0, Method: Composition-based stats.
 Identities = 604/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVFTDNSSPP V PQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+AHG+DPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLAALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct 1567 HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626
 Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHPVTKY
 Sbjct 1627 RLGAVQNEVTLTHPVTKY 1644

> gi|67810868|gb|AA82021.1| polyprotein [Hepatitis C virus]
 Length=1646

Score = 1168 bits (3021), Expect = 0.0, Method: Composition-based stats.
 Identities = 606/618 (98%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
 Sbjct 1029 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 1088

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1089 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1148

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR
 Sbjct 1149 DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR 1208

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1209 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1268

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI
 Sbjct 1269 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 1328

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
 Sbjct 1329 LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 1388

Query 361 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDAL TGYTG
 Sbjct 1389 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALTTGYTG 1448

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgryKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE
 Sbjct 1449 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE 1508

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFW GVFTGLT
 Sbjct 1509 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWGVFTGLT 1568


Query 541 HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
 Sbjct 1569 HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1628

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHPVTKY
 Sbjct 1629 RLGAVQNEVTLTHPVTKY 1646

> gi|67810883|gb|AA82028.1| polyprotein [Hepatitis C virus]
 Length=1644

Score = 1167 bits (3020), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLV+G+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY	
		RLGAVQNEVTLTHPITKY 1644	

> [gi|28921568|ref|NP_803144.1|](#)  NS3 protease/helicase' [Hepatitis C virus]
Length=631

Score = 1167 bits (3019), Expect = 0.0, Method: Composition-based stats.
Identities = 618/631 (97%), Positives = 624/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGVDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEVTLTHPITKYIMTCMSADLEVVT 631	

>gi|67810881|gb|AAY82027.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1167 bits (3019), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAA+TFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAARTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPTCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPPGARSLTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVAMGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQALPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY	
		RLGAVQNEVTLTHPITKY 1644	

> [gi|67810887|gb|AAY82030.1|](#) polyprotein [Hepatitis C virus]
 Length=1644

Score = 1167 bits (3018), Expect = 0.0, Method: Composition-based stats.
 Identities = 602/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEV IVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSR SLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGS IYTYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA+KLVALGINAVAYYRG+DVSVIP GDVVVVATDALMTGYTG	

Sbjct	1387	GGRHLIFCHSKKKKCEDELASKLVALGINAVAYYRGIDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLY	600
		HIDAHFLSQTQKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPRTL GPTPLLY	
Sbjct	1567	HIDAHFLSQTQKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPRTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

>gi|67810844|gb|AA82010.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1166 bits (3016), Expect = 0.0, Method: Composition-based stats.
Identities = 602/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLVLRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSSTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARSSTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDII+CDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTV D E AGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVFDPPENAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY	618
		RLGAVQNE+TLTHP+TKY	
Sbjct	1627	RLGAVQNEVTLTHPITKY	1644

> gi|67810870|gb|AA Y82022.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1165 bits (3013), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRG LLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG LLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRG LLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGP LLC PAGHVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGP LLC PAGHVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLLSPRPISYLGSSGGP LLC PAGHVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI	
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET QDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIETTNASQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY	618
		RLGAVQN +TLTHPVTKY	
Sbjct	1629	RLGAVQNGVTLTHPVTKY	1646

> gi|67810851|gb|AA Y82013.1| polyprotein [Hepatitis C virus]

Length=1644

Score = 1165 bits (3013), Expect = 0.0, Method: Composition-based stats.
Identities = 603/618 (97%), Positives = 609/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARSRLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DGRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+AHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETA ARLVVLATATPPGSVTVPHPNIEEVA STTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAWARLVVLATATPPGSVTVPHPNIEEVAPSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLAALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPT LLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTLLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

> gi|67810896|gb|AA82034.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1164 bits (3010), Expect = 0.0, Method: Composition-based stats.
Identities = 602/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120

Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFNDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFNDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFNDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGS ITYSTYKFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTYKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA+KLVLGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAASKLVTLGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgjrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> gi|67810861|gb|AA82018.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1163 bits (3009), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPTPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1149	DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFNDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFNDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1209	SPVFNDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1268

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKA GIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1329	LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1388
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDS SVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1629	RLGAVQNE+T THPVTKY 1646	

> gi|67810894|gb|AA82033.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 601/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVF TDNSSPPVPQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF TDNSSPP VPQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGS ITYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSK+KCDELA+KLV LGINAVAYYRG+DVSVIP GDV VVVATDALMTG+TG GGRHLIFCHSKRKDELAASKLVTLGINAVAYYRGIDVSVIPTSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> gi|67810864|gb|AAY82019.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 603/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGP L C AGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1149	DSRGSLLSPRPISYLGSSGGP LCLAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPP VPQ FQVAHLHAPTG+GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFETDNSSPPAVPQC FQVAHLHAPTGN GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAE+AGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFC SKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCRSKKKKDELA AKLVALGINAVAYYRGLDVSVIP TSGDV VVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568

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Query   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600
          HIDAHFLSQTKQSGEN PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   1569   HIDAHFLSQTKQSGENFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   1628

Query   601   RLGAVQNEITLTHPVTKY   618
          RLGAVQNE+TLTHPVTKY
Sbjct   1629   RLGAVQNEVTLTHPVTKY   1646

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> gi|68012750|gb|AAV84771.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3004), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

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Query    1   APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct    1   APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60

Query   61   TRTIASPKGPVIQMYTNVDQDLVGWPAQPGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg   120
          T+TIAS KGPVIQMYTNVDQDLVGWPAQPG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   61   TKTIASSKGPVIQMYTNVDQDLVGWPAQPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG   120

Query   121   dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR   180
          DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct   121   DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR   180

Query   181   SPVFSDNSSPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240
          SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   181   SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240

Query   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI   300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI   300

Query   301   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK   360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct   301   LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK   360

Query   361   GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG   420
          GGRHLIFCHSKKKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   361   GGRHLIFCHSKKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG   420

Query   421   DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE   480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRG+TGRGKPGIYRFV PGE
Sbjct   421   DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGKTGRGKPGIYRFVTPGE   480

Query   481   RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT   540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct   481   RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT   540

Query   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600
          HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600

Query   601   RLGAVQNEITLTHPVTKYIMTCMSADLEVVT   631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct   601   RLGAVQNEITLTHPITKYIMTCMSADLEVVT   631

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> gi|68012736|gb|AA84764.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012730|gb|AA84761.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012720|gb|AA84756.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012702|gb|AA84747.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3004), Expect = 0.0, Method: Composition-based stats.
Identities = 615/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVFSNDSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	631

> gi|67810898|gb|AA82035.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 601/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA PVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	PPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGS ITYSTY GKFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTY GKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA+KLV LGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA SKLVTLGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|67810892|gb|AA82032.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 600/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGS ITYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTYKGFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCEDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSK+KCEDELA+KLVLGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKRKCEDELAASKLVTLGINAVAYYRGIDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVCTQTVDVDFSLDPTFTTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNCVCTQTVDVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVCTQTVDVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|68012718|gb|AAV84755.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012716|gb|AAV84754.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012700|gb|AAV84746.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300

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Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
          GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct 361 GGRHLIFCHSKKKKCELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG 420

Query 421 DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct 421 DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT 540

Query 541 HIDAHLFSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
          HIDAHLFSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY
Sbjct 541 HIDAHLFSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

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> [gi|68012706|gb|AAV84749.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012704|gb|AAV84748.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1160 bits (3001), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

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Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct 61 TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct 121 DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180

Query 181 SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA 240
          SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct 181 SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
          GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct 361 GGRHLIFCHSKKKKCELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG 420

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Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEVTLTHPITKYIMTCMSADLEVVT	631

> [gi|68012748|gb|AAY84770.1|](#) nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
 Identities = 615/631 (97%), Positives = 623/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	180
Query	181	SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	

Sbjct 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT

Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012732|gb|AAI84762.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
 Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG

Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 61 TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR

Sbjct 121 DDRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVF+DNSSPP VPQS+QVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA

Sbjct 181 SPVFSDNSSPPAVPQSYQVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI

Sbjct 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK

Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 361 GGRHLIFCHSKKKCDELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG 420

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE

Sbjct 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT

Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT 540

Query 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT

Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012726|gb|AAI84759.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

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Query 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
Sbjct 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
Sbjct 61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121  dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
Sbjct 121  D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR 180

Query 181  SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
Sbjct 181  SPVFSNDSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
Sbjct 241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
Sbjct 301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEIK 360

Query 361  GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
Sbjct 361  GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG 420

Query 421  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE 480
Sbjct 421  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT 540
Sbjct 481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT 540

Query 541  HIDAHLFSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
Sbjct 541  HIDAHLFSQTKQSGENLPY+VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600

Query 601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
Sbjct 601  RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631

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> gi|68012712|gb|AA84752.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2999), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

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Query 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
Sbjct 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
Sbjct 61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

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Query	121	dsrgsls sprPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DCRGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	181	SPVFDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEIK	360
Query	361	GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPPIGDV VVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKCDELA AKLV ALG+NAVAYYRGLDVSVIP GDV VVVVATDALMTG+TG	420
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631	

> gi|68012752|gb|AAY84772.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012742|gb|AAY84767.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012738|gb|AAY84765.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012728|gb|AAY84760.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2998), Expect = 0.0, Method: Composition-based stats.
Identities = 615/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGS RSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsls sprPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240

Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEIK	360
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKKCELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631	

> [gi|68012708|gb|AA84750.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2997), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFSDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEIK	360

Query	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS KKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSNKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> gi|68012698|gb|AAY84745.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2997), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNGDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFSDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	

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Sbjct  481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540
Query   541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
Query   601  RLGAQNEITLTHPVTKYIMTCMSADLEVVT  631
          RLGAQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct   601  RLGAQNEITLTHPITKYIMTCMSADLEVVT  631

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> gi|68012714|gb|AA84753.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2996), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

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Query    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG  60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG  60

Query   61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg  120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG  120

Query   121  dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR  180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct   121  DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR  180

Query   181  SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240
          SPVF+DNSSPP VPQS+QVAHLHA TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   181  SPVFSDNSSPPAVPQSYQVAHLHAATGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240

Query   241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct   241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300

Query   301  LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct   301  LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK  360

Query   361  GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   361  GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG  420

Query   421  DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE  480
          DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct   421  DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE  480

Query   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540

Query   541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600

Query   601  RLGAQNEITLTHPVTKYIMTCMSADLEVVT  631
          RLGAQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct   601  RLGAQNEITLTHPITKYIMTCMSADLEVVT  631

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> gi|68012746|gb|AAY84769.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2995), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFNDNSSPPVVPQSQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSNDSSPPAVPQSYQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVR+RAYMNTPGLPVCQDHLFEWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRVRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

> gi|68012744|gb|AAY84768.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2995), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYL TRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAEATAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKCELAALKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631	

> gi|67810890|gb|AAY82031.1| polyprotein [Hepatitis C virus]

Length=1644

Score = 1157 bits (2994), Expect = 0.0, Method: Composition-based stats.
Identities = 598/618 (96%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTGS ITYST GKFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSSITYSTCGKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK L IGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LDIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCD+LA+KLVA+GINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCDLASKLVAMGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVSLDPTFTTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVSLDPTFTTIET TLPQDAVSRT+RRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVSLDPTFTTIETTTTLPQDAVSRTRRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|89519419|gb|ABD75831.1|](#) polyprotein [Hepatitis C virus]
Length=3008

Score = 1157 bits (2994), Expect = 0.0, Method: Composition-based stats.
Identities = 598/685 (87%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLFSTIITSLTGRDTNENCGEVQVLSTATQSFLGTAINGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPVNQMYTNVDQDLVGWPAPPGVKSLLTPCTCGASDLYLVTRHADVPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RG+LLS RPIS LKGSSGGP L LCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR	180
Sbjct	1147	DTRGALLSARPISTLKGSSGGP L LCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSTPPAVPQAYQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPNIR+GVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK	360
Sbjct	1327	LGIGTVLDQAETAGVRLVLATATPPGSVTTPHSNIEEVALPTTGEVPFYGKAIPLELIK	1386

Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELA KQLTSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
Sbjct	1447	DFDSVIDCNTSVIQTVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGIFDTSVCECYDAGCAWYELTPAETTTRLRAYFNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	600
		ID HFLSQTKQSGEN PYLVA YQATVCARA APPPSWD MWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	QIDGHFLSQTKQSGENFPYLVA YQATVCARALAPPPSWDTMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		VLSG+PAIIPDREVL Y++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVL YQQFDEMEEC 1711	

> gi|68012724|gb|AA Y84758.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 619/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHA TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAATGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLAT TPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATDTPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480

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Sbjct 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE
Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Query 541 HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct 541 HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631
          RLGAVQNEITLTHPITKYIMTCMSADLEVVT

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> gi|68012710|gb|AA84751.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

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Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct 61 TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 120
          TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG
Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct 121 DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180
          DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR
Query 181 SPVF+DNSSPPVPQS+ VAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
          SPVF+DNSSPP VPQS+ VAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct 181 SPVFSDNSSPPAVPQSYPAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
          SPVFSDNSSPPAVPQSYPAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
          YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
          YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI
Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360
          LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK
Query 361 GGRHLIFCHSKKKKCELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
          GGRHLIFCHSKKKKCELAACLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct 361 GGRHLIFCHSKKKKCELAACLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG 420
          GGRHLIFCHSKKKKCELAACLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG
Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE
Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Query 541 HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct 541 HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAHFSLQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY

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Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012722|gb|AA84757.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1156 bits (2991), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct 61 TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct 121 DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
SPVF+DNSSPP VPQS+QVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct 181 SPVFSDNSSPPAVPQSYQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI 300
YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI
Sbjct 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGC SGGAYDIIICDECHSTDATSI 300

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGA L VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct 301 LGIGTVLDQAETAGAILTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
GGRHLIFCHSKKKKCELA AKLVALG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG
Sbjct 361 GGRHLIFCHSKKKKCELA AKLVALGVNAVAYYRGLDVSVIPASGDV VVVATDALMTGFTG 420

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540

Query 541 HIDA HFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 600
HIDA HFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY
Sbjct 541 HIDA HFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012740|gb|AA84766.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1155 bits (2989), Expect = 0.0, Method: Composition-based stats.

Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYL TRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLDRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYILKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYILKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLLSPRPISYILKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLTATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLTATPPGSVTVPHPNIEEVALSTT EIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLTATPPGSVTVPHPNIEEVALSTTVEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

> [gi|89519405|gb|ABD75824.1|](#) polyprotein [Hepatitis C virus]
Length=3009

Score = 1155 bits (2987), Expect = 0.0, Method: Composition-based stats.
Identities = 598/685 (87%), Positives = 642/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL IITSLSLTGRD N+ GEVQ++STA Q+FL T +NGV WTVYHGAG	
Sbjct	1028	APITAYAQQTRGLFSTIITSLSLTGRDNTNENCGEVQVLSTATQSFLGTAVNGVMWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	
Sbjct	1088	SKTISGPKGPVNQMYTNVDQDLVGWPAPPVKSLTPCTCGASDLYLVTRHADVVPVRRRG	1147

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1148	D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR DTRGALLSPRPIS TLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1208	SPVFTDNS+PP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSTPPAVPQTYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1268	YMSKA+GIDPNIR+GVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAYGIDPNIRSGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1328	LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK LGIGTVLDQAETAGVRLVVLATATPPGSVTTPHSNIEEVALPTTGEVPFYGKAIPLELIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1388	GGRHLIFCHSKKKCDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG GGRHLIFCHSKKKCDELA KQLTSLGLNAVAYYRGLDVSVIPTSGDV VVCATDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1448	DFDSVIDCNT V QTVD FSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE DFDSVIDCNTSVIQTVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1508	RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT RPSGIFDTSVCECYDAGCAWYELTPAETTRLRAYFNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1568	ID HFLSQTKQSGEN PYL VAYQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY QIDGHFLSQTKQSGENFPYL VAYQATVCARALAPPPSWDTMWKCLIRLKPTLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1628	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCLS G VVIVGRV RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLSVGSVVIVGRV	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1688	VLSG+PAIIPDREVLY++FDEMEEC VLSGQPAIIPDREVLYQQFDEMEEC	1712

> gi|89519409|gb|ABD75826.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1154 bits (2984), Expect = 0.0, Method: Composition-based stats.
Identities = 599/685 (87%), Positives = 643/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	AP+TAYAQQTRGL+ IITSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG APVTAYAQQTRGLVNTIITSLTGRDNTNENCGEVQVLSTATQSFLGTAINGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG SKTISGPKGPVNQMYTNVDQDLVGWPAPPVGVKSLTPCTCGASDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDFIPVE+L TTMR DTRGALLSPRPIS TLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFIPVESLATTTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct		SPVFTDNS+PP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSTPPAVPQAYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RLVLATATPPGSVT PH NIEEVAL TTGEIPFYGKAIPLE+IK	360
Sbjct	1327	LGIGTVLDQAETAGVRLVLATATPPGSVTTPHSNIEEVALPTTGEIPFYGKAIPLELIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCE+A +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCEVANQLKSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTSVIQTVDFSLDPTFSIETTTIPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGIFDTSVICCYDAGCAWYELTPAETTURLRAYFNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY ID HFLSQTKQSGEN PYLVAQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	QIDGHFLSQTKQSGENFPYLVAQATVCARALAPPPSWDMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	660
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSG+PAIIPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVLYQQFDEMEEC 1711	

> [gi|68012694|gb|AA84743.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1153 bits (2983), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 618/631 (97%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DGRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRPGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLK TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKTTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> gi|68012696|gb|AA84744.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1153 bits (2982), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 618/631 (97%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWT YHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTGYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPTCTGSSDLVLRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPTCTGSSDLVLRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNGDQDLVGWPAPQGARSLTPTCTGSSDLVLRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	

Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLK TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

>gi|67810885|gb|AA82029.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1152 bits (2981), Expect = 0.0, Method: Composition-based stats.
Identities = 599/618 (96%), Positives = 605/618 (97%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQ EGEVQIVSTAAQTFLATCINGVCWTVY GAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQAEGEVQIVSTAAQTFLATCINGVCWTVYRGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYT+VD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTDVDDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFG	
Sbjct	1207	SPVFTDNSSPPAVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGT	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGS ITYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSSITYSTYKGFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA+KLVALGINAVAYYRG+DVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAASKLVALGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGK GIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSRTQRRGRTGRGKLG IYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+ LTHP+TKY
 Sbjct 1627 RLGAVQNEVILTHPITKY 1644

> gi|89519413|gb|ABD75828.1| polyprotein [Hepatitis C virus]
 Length=3007

Score = 1151 bits (2977), Expect = 0.0, Method: Composition-based stats.
 Identities = 590/685 (86%), Positives = 644/685 (94%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG+LG IITSLSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG	
Sbjct	1026	APITAYAQQTRGMLGTIITSLSLTGRDNTNENCGEVQVLSTATQSFLGTAINGVMWTVYHGAG	1085
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCGSSDL+LVTR+ADV+P+RRRG	
Sbjct	1086	SKTISGPKGPVNQMYTNVDQDLVGWPAPPVGVKSLTPCTCGSSDLFLVTRNADVVPPLRRRG	1145
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RG+L+SPRPIS LKGSSGGPLLCP GHA GIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1146	DTRGALISPRPISTLKGSSGGPLLCPGLHAAGIFRAAVCTRGVAKAVDFVPVESLETTMR	1205
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1206	SPVFTDNSTPPAVPQTYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1265
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIR+GVRTITTTG+PITYSTY GKFLADGGC+GGAYDIIICDECHSTDAT++	
Sbjct	1266	YMSKAHGIDPNIRSGVRTITTTGAPITYSTY GKFLADGGCAGGAYDIIICDECHSTDATTV	1325
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVT PH NIEEVAL TTGEIPFYGKA IPL ++K	
Sbjct	1326	LGIGTVLDQAETAGARLVVLATATPPGSVTTPHSNIEEVALPTTGEIPFYGKA IPLSLVK	1385
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
Sbjct	1386	GGRHLIFCHSKKKKCELAQLSSLGLNAVAYYRGLDVSVIPLSGDVVVCATDALMTGFTG	1445
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFD+VIDCNT V QTVD FSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
Sbjct	1446	DFDTVIDCNTSVIQTVDFSLDPTFTSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1505
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSG+FD+SVLCECYD GCAWYELTPAETT+RLRAY NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1506	RPSGIFDTSVLCECYDTGCAWYELTPAETTIRLRAYFNT PGLPVCQDHLEFWESVFTGLT	1565
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HID HFLSQTKQ+G+N PYL VAYQATVCA+A APPPSWD MWKCL+RLKPTL GPTPLLY	
Sbjct	1566	HIDGHFLSQTKQAGDNFPYL VAYQATVCAKALAPPPSWDTMWKCLLRLKPTLRGPTPLLY	1625
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlggylaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWV+VGG+LAALAAAYCLS G VVIVGRV	
Sbjct	1626	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVMVGGLLAALAAAYCLSVGSVVIVGRV	1685
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSG+PA+IPDREVLY++FDEMEEC	
Sbjct	1686	VLSGQPAVIPDREVLYKQFDEMEEC	1710

> gi|89519407|gb|ABD75825.1| polyprotein [Hepatitis C virus]

Length=3008

Score = 1151 bits (2977), Expect = 0.0, Method: Composition-based stats.
Identities = 595/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL T +NGV WTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYL+TRHADV+PVRRRG	1146
Query	121	dsrgslsaprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRP+S LKGSSGGPLLCP GHA G FRAAVCTRGVAKAVDF+PVE+LETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYA+QGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	ID HFLSQTKQSGEN PYLVAQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	VLSG+PAIIPDREVLY++FDEMEEC 1711	

>gi|89519415|gb|ABD75829.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 593/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAYAQQTRGL I+TSLTG+D N+ GEVQ++STA Q+FL T +NGV W+VYHGAG APITAYAQQTRGLFSTIVTSLTGKDTNENCGEVQVLSTATQSFGLGTAVNGVMWSVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPVNQMYTNVDQDLVGWPAPPVKSRLTPCTCGASDLYLVRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR	180
Sbjct	1147	DTRGALLSPRPISTLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFOVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSTPPAVPQTYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPNIR+GVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVT PH NIEE+AL TTGEIPFYG+AIPL++IK	360
Sbjct	1327	LGIGTVLDQAETAGVRLTVLATATPPGSVTTPHSNIEEIALPTTGEIPFYGRAIPLDLIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKDELA +L ALG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAQLTALGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTSVIQTVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWGVFTGLT RPSG+FD+SVLCECYDAGCAWYELTPAETT RLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGIFDTSVLCECYDAGCAWYELTPAETTTRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY ID HFLSQTKQSGEN PYLVAQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	QIDGHFLSQTKQSGENFPYLVAQATVCARALAPPPSWDTMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVI GRV	660
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSVVITGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSG+PAIIPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVLYQQFDEMEEC 1711	

>gi|89519411|gb|ABD75827.1| polyprotein [Hepatitis C virus]
Length=2985

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 593/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL +NGV WTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLFSTIITSLTGRDTNENCGEVQVLSTATQSFGLGVAVNGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++TI+ PKGP+ QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYL+TRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPINQMYTNVDQDLVGWPAPPVKSRLTPCTCGASDLYLITRHADVVPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRPIS LKGSSGGPLLCP GHA GIFRAAVCTRGVAKAVDF+PVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF+DNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYA QGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKFLADGGC GGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAG RLVLATATPPGSVT PH NIEEVAL TTGEIPFYGKAIP++IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSG+FD+SVLCECYDAGCAWYELTP+ETT+RLRAY+NTPGLPVCQDHLEFWE VFTGL	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	ID HFLSQTKQSGENLPYLVA YQATVCARA APPPSWD MW+CLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSG+PAIIPDREVLYR+FDEMEEC	1711

> [gi|81924266|sp|O91936|POLG_HCVSA](#) Genome polyprotein [Contains: Core protein p21 (C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|3660726|gb|AAC61696.1|](#) polyprotein [Hepatitis C virus (isolate SA13)]
 Length=3014

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
 Identities = 585/685 (85%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1028	APITAYAQQTRG+LG II SLTGRDKN+ EGEVQ++STA QTFL TCINGV WTV+HGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+T+A PKGPV+QMYTNVD+DLVGWP P G+RSLTPCTCGS+DLYLVTRHADV+P RRRG	

Sbjct	1088	AKTLAGPKGPVVQMYTNVDKDLVGWPTPPGTRSLTPCTCGSADLYLVTRHADVVPARRRG	1147
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+R SLLSPRPISYLGSSGGP++CP+GH VG+FRAAVCTRGVAKA+DFIPVENLETTMR	
Sbjct	1148	DTRASLLSPRPISYLGSSGGPVMCPSPGHVVGVFRAAVCTRGVAKALDFIPVENLETTMR	1207
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VP FQV HLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1208	SPVFTDNSTPPAVPHEFQVGH LHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+A+G+DPNIRTGVRT+TTG+ ITYSTY GKFLADGGCSGGAYD+IICDECHS DAT+I	
Sbjct	1268	YMSRAYGVDPNIRTGVRTVTTGAAITYSTY GKFLADGGCSGGAYDVIICDECHSQDATTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVT PHPNIEEVAL + GEIPFYG+AIPL +IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTTTPHPNIEEVALPSEGEIPFYGRAIPLALIK	1387
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIPPIDGVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA +L + G+NAVAYYRGLDV+VIP GDVVV +TDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKKCELA KQLTSQGVNAVAYYRGLDVAVIPATGDVVVCSTDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTT IETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNT VTQTVD FSLDPTFTT IET T+PQDAVSR+QRRGRTGRG+ GIYR+V+ GE	
Sbjct	1448	DFDSVIDCNTT VTTQTVD FSLDPTFTT IETTTVPQDAVSRSQRRGRTGRGRHGIYRVSSGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSG+FDS VLCECYDAGCAWY+LTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1508	RPSGIFDSSVLCECYDAGCAWYDLTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		+IDAH LSQTKQ GEN PYL VAYQATVC RA+APPPSWD MWKC++RLKPTL GPTPLLY	
Sbjct	1568	NIDAHMLSQTKQGGENFPYL VAYQATVCVRAKAPPPSWDMWKMLRLKPTLTGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TKYIM CMSADLEV+TSTWVLVGGV+AALAAAYCL+ G V IVGR+	
Sbjct	1628	RLGAVQNEITLTHPITKYIMACMSADLEVITSTWVLVGGVVAALAAAYCLTVGSVAIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PAIIPDREVLY++FDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVLYQQFDEMEEC	1712

>gi|68012734|gb|AA84763.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 619/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPA HAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAVHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSNDSPPAVPQSYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDP IRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPIIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGI TVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIDTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSVSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSVSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSVSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

>gi|89519417|gb|ABD75830.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1149 bits (2973), Expect = 0.0, Method: Composition-based stats.
Identities = 594/685 (86%), Positives = 640/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL I+TSLTGRD N+ GEVQ++STA Q+FL T +NGV W+VYHGAG	
Sbjct	1027	APITAYAQQTRGLFSTIVTSLTGRDNTNENCGEVQVLSTATQSFLGTAVNGVMWSVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	
Sbjct	1087	GKTISGPKGPVNQMYTNVDQDLVGWPAPPGVKSRLTPCTCGASDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RG+LLSPRPIS LKGSSGGPLLC P GH G+FRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DTRGALLSPRPISLTLKGSSGGPLLCMPGHVAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEE+AL TTGEIPFYGKAIPLE+IK	

Sbjct	1327	LGIGTVLDQAETAGVRLVVLATATPPGSVTTPHSNIEEIALPTTGEIPFYGKAIPLELIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAQQLTSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTSVIQTVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWGVFTGLT RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGIFDTSVCECYDAGCAWYELTPAETTTTLRAYFNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY ID HFLSQTKQSGEN PYL VAYQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	QIDGHFLSQTKQSGENFPYL VAYQATVCARALAPPPSWDMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	660
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSG+PA+IPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAVIPDREVLYQQFDEMEEC 1711	

>[gi|3550759|dbj|BAA32664.1| polyprotein [Hepatitis C virus (isolate Th580)]
gi|81924482|sp|O92529|POLG HCVT5 Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
Length=3019

Score = 1146 bits (2965), Expect = 0.0, Method: Composition-based stats.
Identities = 586/685 (85%), Positives = 633/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+ EGEVQ+VSTA Q+FLAT INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKN EAGEVQVSTATQSFLATTINGVLWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++ +A PKGPV QMYTNVDQDLVGWPAP G+RSL PCTCGSSDLYLVTR ADVIP RRRG	120
Sbjct	1092	SKNLAGPKGPVCQMYTNVDQDLVGWPAPLGARSLAPCTCGSSDLYLVTRGADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGS SGGPL+CP+GH VG+FRAAVCTRGVAKA+DFIPVEN++TTMR	180
Sbjct	1152	DTRAALLSPRPIS TLKGS SGGPLMCPSGHVGLFRAAVCTRGVAKALDFIPVENMDTTMR	1211
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ++QV +LHAPTGS GKST+VPAAYA QGYKVLVLNPSVAATL FGA	240
Sbjct	1212	SPVFTDNSSPPAVPQTYQVGYLHAPTGS GKSTRVPAAYATQGYKVLVLNPSVAATLSFGA	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKF LADGGC SGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG P+TYSTY GKF LADGGC SGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMSKAHGIDPNIRTGVRTITTTGGPVTYSTY GKF LADGGC SGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1332	LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I E AL TTGEIPFYGK IPLE IK LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKIPLEFIK	1391
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVA+YRG+DV+VIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKKCELSKQLTSLGLNAVAFYRGVDVAVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDS SVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDS VLCE YD GCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDSVVLCEAYDTGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ GEN YLVA YQATVCARA+APPPSWD MWKCL RLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVA YQATVCARAKAPPPSWDMWKCLTRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWV+VGGVLAALAAAYCL+ GCVVI GR+	660
Sbjct	1632	RLGAVQNEIVTTHPITKYIMTCMSADLEVITSTWVIVGGVLAALAAAYCLTVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 V SGKPA++PDREVLY++FDEMEEC	
Sbjct	1692	VTSGKPAVVPDREVLYQQFDEMEEC 1716	

>gi|73765377|gb|AAZ85046.1| polyprotein [Hepatitis C virus]
Length=3012

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 578/685 (84%), Positives = 634/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY QQTRGLLG I+TSLTGRDKN+VEGE+Q+VSTA QTFLAT +NGV WTVYHGAG	60
Sbjct	1034	APITAYHQQTRGLLGTIVTSLTGRDKNVEGEIQVSTATQTFLATAVNGVLWTVYHGAG	1093
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQD+VGWPAP G+RSLTPCTCGSSD+YLVTR+ADVIP RRRG	120
Sbjct	1094	SKTLAGPKGPVCQMYTNVDQDMVGWPAPPGARSRLTPCTCGSSDVYLVTRNADVIPARRRG	1153
Query	121	dsrgsllsprPISYLGSSGGPILCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R LLSPRP+S LKGSSGGP+LCP+GHAVG+FRAAVCTRGVAKA+DF+PVEN+ETTMR	180
Sbjct	1154	DTRAGLLSPRPLSTLKGSSGGPILCPSGHAVGLFRAAVCTRGVAKAIDFVPVENMETTMR	1213
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VP ++QV +LHAPTGS GKSTKVPAAAY+QGYKVLVLNPSVAATL FG+	240
Sbjct	1214	SPVFTDNSSPPAVPSTYQVGYLHAPTGS GKSTKVPAAAYASQGYKVLVLNPSVAATLAFGS	1273
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG PITYSTY GKFLADGGCSGGAYDIIICDECHSTD T+I	300
Sbjct	1274	YMSKAHGVDPNIRTGVRTITTTGGPITYSTY GKFLADGGCSGGAYDIIICDECHSTDPTTI	1333
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I EVAL TTGE+PFY G+ IPLE IK	360
Sbjct	1334	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNISEVALPTTGEVPPFYGRGIPLEYIK	1393
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1394	GGRHLIFCHSKKKKCELAQLRSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1453

Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1454	DFDSVIDCN VTQ VDFSLDPTFTIET T+PQDAV+R+QRRGRTGRGKPG+YR+V+ GE	1513
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1514	RPSGTFDTVVLC EAYDVGCAWYELTPSETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1573
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1574	HIDAHFLSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCL+RLKP L GPTPLLY	1633
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1634	RLGAVQNE+T THP+TKYIMTCMSADLEV+TS WVL GG+LAALAAAYCL+TG VI GR+	1693
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1694	+ SGKPA++PDREVLY++FDEMEEC	1718

>gi|93102510|gb|ABE98157.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 635/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1032	APITAYAQQTRGL G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVT RHADVIPVrrrg	120
Sbjct	1092	+RT+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVT R ADVIP RRRG	1151
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1152	D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DF+PVEN+ETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1212	SP FTDNS+PP VPQ++QV +LHAPTSGSKST+VPAAYA QGYKVLVLNPSVAATL FG+	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1272	YM +A+G++PN+RTGVRT+TTG ITYSTY GKFLADGGCSGGAYDIIICDECHSTD T++	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1332	LGIGTVLDQAE+AG RL VLATATPPGSVTVPHPNI E ALSTTGEIPFYGKAIPLE IK	1391
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1452	DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1512	RPSGMFDS VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK GEN YLVAIQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTQKQGENFAYLVAIQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	660
Sbjct	1632	RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 L+GKPA++PDRE+LY++FDEMEEC	
Sbjct	1692	TLTGKPAVVPDREILYQQFDEMEEC 1716	

>gi|93102504|gb|ABE98154.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1144 bits (2958), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FL T INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLVTSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVD+D+VGWP+P G+RSLTPCTCGSSDLYLVTR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDVVGWPSPPGARSRLTPCTCGSSDLYLVTTREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FAAVCTRGVAK++DFIPVEN+ETMR	180
Sbjct	1152	DNRAALLSPRPISTLKGSSGGPIMCPSGHVVLGFAAVCTRGVAKSLDFIPVENMETMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVLNPSVAATL FG+	240
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YM +A+G++PNIRTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMRQAYGVEPNIRTGVRTVTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E ALSTTGEIPFYGKAIPLE IK	360
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKCDELA AKLRSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVVDFSLDPTFSIETTTVPQDAVSRQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK GEN YLVAIQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTQKQGENFAYLVAIQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631

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Query 601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV 660
           RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct 1632 RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661  VLSGKPAIIPDREVLVREFDEMEEC 685
           L+GKPA++PDRE+LY++FDEMEEC
Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

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>gi|93102494|gb|ABE98149.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1142 bits (2955), Expect = 0.0, Method: Composition-based stats.
Identities = 579/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

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Query 1  APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG
Sbjct 1032 APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG 1091

Query 61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
          ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVR ADVIP RRRG
Sbjct 1092 SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLVTREADVIPARRRG 1151

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
          D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FAAVCTRGVAK++DFIPVEN+ETTMR
Sbjct 1152 DNRAALLSPRPISTLKGSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR 1211

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
          SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVLNPSVAATL FG+
Sbjct 1212 SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVLNPSVAATLSFGS 1271

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
          YM +A+G++PN+RTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++
Sbjct 1272 YMRQAYGVEPNVRTGVRTVTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV 1331

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
          LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E ALSTTGEIPFYGKAIPLE IK
Sbjct 1332 LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK 1391

Query 361 GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
          GGRHLIFCHSKKKCDELA +L +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
Sbjct 1392 GGRHLIFCHSKKKCDELAGQLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG 1451

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
          DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRR RTGRGKPG+YR V+ GE
Sbjct 1452 DFDSVIDCNVAVTQVVD FSLDPTFSIETTTVPQDAVSRQRRVRTGRGKPGVYRIVSQGE 1511

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT
Sbjct 1512 RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 1571

Query 541 HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY 600
          HIDAHFLSQTKQ GEN YLVA YQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY
Sbjct 1572 HIDAHFLSQTKQGGENFAYLVA YQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY 1631

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV 660
          RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct 1632 RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685

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L+GKPA++PDRE+LY++FDEMEEC

Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

> [gi|81985682|sp|Q5I2N3|POLG_HCV6A](#) Genome polyprotein [Contains: Core protein p21 (C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|57791994|gb|AAW56714.1|](#) polyprotein [Hepatitis C virus (isolate 6a33)]
 Length=3019

Score = 1142 bits (2955), Expect = 0.0, Method: Composition-based stats.
 Identities = 579/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVTR ADVIP RRRG	
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSRLTPCTCGSSDLYLVTTREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLGSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FAAVCTRGVAK++DFIPVEN+ETTMR	
Sbjct	1152	DNRAALLSPRPISTLKGSSSGGPVMCPSGHVVLFRFAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVNLPSVAATL FG+	
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVNLPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YM +A+G++PN+RTGVRT+TTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD T++	
Sbjct	1272	YMRQAYGVEPNVRTGVRTVTTGGAITYSTYKGFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGS+TVPHPN I E AL TTGEIPFYGKAIPLE IK	
Sbjct	1332	LGIGTVLDQAETAGARLTVLATATPPGSITVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVV+ ATDALMTGYTG	
Sbjct	1392	GGRHLIFCHSKKKKDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVICATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	
Sbjct	1452	DFDSVIDCNVAVTQVVDVDFSLDPTFSIETTTVPQDAVSRQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFD+ VLCE YD GCAWYELTP+ETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ GEN YLVAQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVAQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	
Sbjct	1632	RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 L+GKPA++PDRE+LY++FDEMEEC
 Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

>gi|93102500|gb|ABE98152.1| polyprotein [Hepatitis C virus subtype 6a]
 Length=3019

Score = 1142 bits (2953), Expect = 0.0, Method: Composition-based stats.
 Identities = 582/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT +NGV WTVYHGAG
 Sbjct 1032 APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSVNGVMWTVYHGAG 1091

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
 ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVR ADVIP RRRG
 Sbjct 1092 SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSRLTPCTCGSSDLYLVTREADVIPARRRG 1151

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTM
 Sbjct 1152 DNRAALLSPRPISLTKGSSGGPIMCPSGHVVGIFRAAVCTRGVAKSLDFIPVENMETTMR 1211

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SP FTDNS+PP VPQ++QV +LHAPTGSKGST+VPAAYA+QGYKVLVNLNPSVAATL FG+
 Sbjct 1212 SPSFTDNSTPPAVPQTYQVGYLHAPTGSKGSTRVPAAYASQGYKVLVNLNPSVAATLSFGS 1271

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YM +AHG++PNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD T++
 Sbjct 1272 YMRQAHGVEPNIRTGVRTITTTGGAITYSTYKGFLADGGCSGGAYDIIICDECHSTDPTTV 1331

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK
 Sbjct 1332 LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK 1391

Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
 Sbjct 1392 GGRHLIFCHSKKKKDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG 1451

Query 421 DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgKPGIYRFVAPGE 480
 DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE
 Sbjct 1452 DFDSVIDCNVAVTQVVDVDFSLDPTFSIETTTVPQDAVSRQRRGRTGRGKPGVYRFVSQGE 1511

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT 540
 RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT
 Sbjct 1512 RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT 1571

Query 541 HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTQKQ GEN YLVAQATVCARA+APPPSWD MWKCLIRLKP TL GPTPLLY
 Sbjct 1572 HIDAFLSQTQKQGENFAYLVAYQATVCARAKAPPPSWDMWKCLIRLKP TLTGPTPLLY 1631

Query 601 RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV 660
 RLGAVQNEI THP+TKYIMTMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
 Sbjct 1632 RLGAVQNEIITHPITKYIMTMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 L+GKPA++PDRE+LY++FDEMEEC
 Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

>gi|93102492|gb|ABE98148.1| polyprotein [Hepatitis C virus subtype 6a]

Length=3019

Score = 1140 bits (2950), Expect = 0.0, Method: Composition-based stats..
Identities = 581/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

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Query 1      APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
              APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG
Sbjct 1032   APITAYAQQTRGLVGTIVTSLTGRDKNQVEGEVQVVSTATQSFLATSINGVMWTVYHGAG 1091

Query 61     TRTIASPKGPVIQMYTNVDQDLVGWPAPOGSRSLTPCTCGSSDLYLVRHADVIPVrrrg 120
              ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVR ADVIP RRRG
Sbjct 1092   SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLVTREADVIPARRRG 1151

Query 121    dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
              D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR
Sbjct 1152   DNRAALLSPRPISLTKGSSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR 1211

Query 181    SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
              SP FTDNS+PP VPQ++QV +LHAPTGSGBKST+VPAAYA+QGYKVLVNLNPSVAATL FG+
Sbjct 1212   SPSFTDNSTPPAVPQTYQVGYLHAPTGSBKSTRVPAAYASQGYKVLVNLNPSVAATLSFGS 1271

Query 241    YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
              YM +A+G++PN+RTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++
Sbjct 1272   YMRQAYGVEPNVRTGVRTVTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV 1331

Query 301    LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
              LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I E ALSTTGEIPFYGKAIPLE IK
Sbjct 1332   LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK 1391

Query 361    GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
              GGRHLIFCHSKKKKCELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
Sbjct 1392   GGRHLIFCHSKKKKCELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG 1451

Query 421    DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
              DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE
Sbjct 1452   DFDSVIDCNVAVTQVVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE 1511

Query 481    RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
              RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT
Sbjct 1512   RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 1571

Query 541    HIDAHLFSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
              HIDAHLFSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCLIRLKP TL GPTPLLY
Sbjct 1572   HIDAHLFSQTKQGENFAYLVAYQATVCARAKAPPPSWDTMWKCLIRLKP TLTGPTPLLY 1631

Query 601    RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV 660
              RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct 1632   RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661    VLSGKPAIIPDREVLRYREFDEMEEC 685
              L+GKPA++PDRE+LY++FDEMEEC
Sbjct 1692   TLTGKPAVVPDREILYQQFDEMEEC 1716

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> [gi|93102502|gb|ABE98153.1|](#) polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1140 bits (2948), Expect = 0.0, Method: Composition-based stats..
Identities = 581/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

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Query 1      APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

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Sbjct	1032	APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYL+TR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLITREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKSSGGPPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR	180
Sbjct	1152	DNRAALLSPRPIS TLKGSSGGPIMCPSGHVVLFRAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVNLNPSVAATL FG+	240
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVNLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YM +A+G++PNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMRQAYGVEPNIRTGVRTITTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK	360
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKKDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKKDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFD+ VLCE YD GCAWYELTP+ETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ GEN YL VAYQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVAYQATVCARAKAPPPSWDIMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	660
Sbjct	1632	RLGAVQNEIITHPITKYIMTMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 L+GKPA++PDRE+LY++FDEMEEC	
Sbjct	1692	TLTGKPAVVPDREILYQQFDEMEEC 1716	

>gi|93102514|gb|ABE98159.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1139 bits (2947), Expect = 0.0, Method: Composition-based stats.
Identities = 580/685 (84%), Positives = 635/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWP+P G+RSLTPCTCGS+DLYLVTR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDQDLVGWPSPPGARSLTPCTCGSNDLYLVTRADVIPARRRG	1151

Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSR +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTM	
Sbjct	1152	DSRAALLSPRPISLTKGSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQSFFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SP FTDNS+PP VPQ++QV +LHAPTGSKGST+VPAAYA+QGYKVLVLNPSVAATL FG+	
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGSKGSTRVPAAYASQGYKVLVLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YM +A+G++PN+RTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD T++	
Sbjct	1272	YMRQAYGVEPNVRTGVRTITTTGGAITYSTYKGFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK	
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	
Sbjct	1392	GGRHLIFCHSKKKKCELAGKLSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	
Sbjct	1452	DFDSVIDCNVAVTQVVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFD+ VLCE YD GCAWYELTP+ETT VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1512	RPSGMFDTVVLCAYDTGCAWYELTPSETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVAYQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI THP+TKYIMTCSADLEV+TSTWV+VGGVLAALAAAYCLS GCVVI GR+	
Sbjct	1632	RLGAVQNEIITTHPITKYIMTCSADLEVITSTWVIVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		L+GKP ++PDREVLY++FDEMEEC	
Sbjct	1692	TLTGKPVVVPDREVLYQQFDEMEEC	1716

Get selected sequences

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Distance tree of results

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jul 20, 2006 3:05 AM

Number of letters in database: 1,312,134,661

Number of sequences in database: 3,805,897

Lambda K H
0.320 0.136 0.423

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 3805897

Number of Hits to DB: 171000343

Number of extensions: 7142453

Number of successful extensions: 17341
Number of sequences better than 10: 85
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 17304
Number of HSP's successfully gapped: 85
Length of query: 685
Length of database: 1312134661
Length adjustment: 137
Effective length of query: 548
Effective length of database: 790726772
Effective search space: 433318271056
Effective search space used: 433318271056
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (20.4 bits)
S2: 80 (35.4 bits)